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Fr m: Jiang, Dong
Sent: Friday, January 10, 2003 6:05 PM
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Subject: 09/931,836

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Please search 1) SEQ ID NO:2

-issued
-commercial

STIC-Biotech
Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).
Thank you very much.

Dong Jiang (78243)
703-305-1345
U.S. Patent and Trademark Office
Art Unit 1646
dong.jiang@uspto.gov
CM1-10D08
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Searcher: _____
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Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:31:23 : Search time 36 Seconds
(without alignments)
910.546 Million cell updates/sec

Title: US-09-931-836-2

Perfect score: 1367

Sequence: 1 MLNRQLIYWOLLALFLPFC.....LHGDHQRFSTFAGFLIFETK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1367	100.0	246	21	AA15548 Human immune syste
2	1367	100.0	246	21	AA15548 Human adipocyte co
3	1367	100.0	246	21	AA181909 A novel polypeptid
4	1367	100.0	246	22	AA188447 Human membrane or
5	1367	100.0	246	23	AA184371 Novel human secret
6	1320.5	96.6	319	23	AA184370 Novel human secret
7	1311	95.9	246	21	AA129582 Mouse zacr2 prote
8	1208	88.4	225	22	AA199925 Human polypeptide
9	884	64.7	202	22	AA141860 Human polypeptide
10	792.5	58.0	223	22	AA106589 Human protein havi

11	721	52.7	128	20	AA11485 Human 5' EST sece
12	663	48.5	126	22	AA140074 Human polypeptide
13	582	42.6	105	21	AA175969 Rat skin cell prot
14	582	42.6	105	21	AA175969 Rat skin cell prot
15	582	42.6	105	22	AA155908 Skin cell protein,
16	582	42.6	105	22	AA155908 Skin cell protein,
17	582	42.6	105	22	AA155908 Skin cell protein,
18	582	42.6	105	23	AA172108 Rat protein isolat
19	582	42.6	105	23	AA172108 Rat protein isolat
20	325	23.8	267	23	AA184378 Novel human secret
21	319	23.3	285	21	AA176103 Rat skin cell secr
22	319	23.3	285	22	AA156042 Skin cell protein,
23	316	23.1	294	21	AA172242 Rat protein isolat
24	316	23.1	294	21	AA176039 Rat skin cell prot
25	316	23.1	294	23	AA155978 Skin cell protein,
26	315.5	23.1	288	22	AA172178 Rat protein isolat
27	315	23.0	289	23	AA109443 Human SHACRP30a p
28	315	23.0	289	23	AA109443 Human novel polype
29	315	23.0	296	23	AA101524 Novel human protei
30	315	23.0	303	22	AA109444 Human ganset metab
31	315	23.0	303	22	AA109444 Human SHACRP30a p
32	313	22.9	285	21	AA150371 Human ZACRP7, Hom
33	309	22.6	289	22	AA150371 Murine ZACRP7, Mus
34	308	22.5	289	23	AA172306 Rat protein isolat
35	306	22.4	314	23	AA141487 Human ovarian anti
36	306	22.4	331	22	AA119557 Human diagnostic a
37	304	22.2	285	21	AA130232 Human adipocyte co
38	304	22.2	285	21	AA130232 A polypeptide desi
39	304	22.2	285	22	AA150374 Human adipocyte co
40	297.5	21.8	225	23	AA180583 Human sbg103026C1
41	297.5	21.8	244	18	AA190108 Human adipocyte co
42	296.5	21.7	260	21	AA191522 Human secreted pro
43	296.5	21.7	287	21	AA191666 Human secreted pro
44	294	21.5	247	18	AA109107 Murine adipocyte c
45	294	21.5	247	22	AA105528 Mouse OBG3 protein

ALIGNMENTS

RESULT 1

AA15548

ID AA15548 standard; Protein; 246 AA.

XX AA15548;

AC AA15548;

XX 28-FEB-2001 (first entry)

DT 28-FEB-2001 (first entry)

XX Human immune system molecule from Incyte clone 1890540.

XX Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;

KW antiarteriosclerotic; antidiabetic; antidiabetic; nephrotropic; cancer;

KW Antitumor; dermatological; antithyroid; virucide; hepatotropic; antibody;

KW immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;

KW gene therapy; diagnostic; immunological disorder; viral infection;

KW bacterial infection; fungal infection; parasitic infection; immunogen.

XX Homo sapiens.

OS Homo sapiens.

XX WO2000060080-A2.

XX 12-OCT-2000.

XX 04-APR-2000; 2000WO-US09072.

XX 05-APR-1999; 99US-0127852.

XX 05-MAY-1999; 99US-0132647.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Lal P, Tang Y, Baughn MR, Azimzai Y, Lu DAM;

XX WPI; 2000-665005/64.

XX

XX

XX

XX

DR N-PSDB; AAA95787.
XX New human immune system molecules 1-15 and polynucleotides encoding
PT them useful for diagnosing, treating or preventing e.g. immunological
PT disorders, infections, cell proliferative disorders, microbial
PT infections -
XX
PS Claim 1; Page 85; 95pp; English.
XX
XX This sequence represents a human immune system molecule (IMOL) encoded
CC by the cDNA isolated as clone 1890540 from the Incyte BLADU07 library.
CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides
CC (AAA95775-A95789), and compositions comprising them are useful for the
CC diagnosis, treatment or prevention of immunological disorders,
CC infections and cell proliferative disorders, including cancer. The IMOL
CC may be used to treat or prevent disorders associated with decreased
CC expression or activity of IMOL, such as immunological disorders
CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,
CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.
CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and
CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
CC useful as immunogens for the development of antibodies that
CC specifically recognize these peptides. The polynucleotides may be used
CC to detect and quantify gene expression in biopsied tissues in which
CC expression of IMOL may be correlated with the disease as targets in a
CC microarray, to detect differences in gene sequences among normal,
CC carrier and affected individuals, and for screening libraries of
CC compounds in drug screening techniques. Antibodies which specifically
CC bind to IMOL may be used for the diagnosis of disorders characterized
CC by expression of IMOL, or in assays to monitor patients being treated
CC with IMOL or agonists, antagonists, or inhibitors of IMOL.
XX
XX Sequence 246 AA;

Query Match 100.0%; Score 1367; DB 21; Length 246;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWRQLIYWQLLALFFLPCLCODEYMESFQTGLPPDCSKCHGYSFRGYGPPGPG 60
DB 1 MLWRQLIYWQLLALFFLPCLCODEYMESFQTGLPPDCSKCHGYSFRGYGPPGPG 60
QY 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120
DB 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120
QY 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRGAPVSGVYFFTFMSMKHEDVEEYV 180
DB 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRGAPVSGVYFFTFMSMKHEDVEEYV 180
QY 181 YLMHNGNTVFSMYSYEMKKGSDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRFSFAGF 240
DB 181 YLMHNGNTVFSMYSYEMKKGSDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRFSFAGF 240
QY 241 LLEFETK 246
DB 241 LLEFETK 246

RESULT 2
ID AAB29580
XX AAB29580 standard; Protein; 246 AA.
AC AAB29580;
XX
XX 19-FEB-2001 (first entry)
DT
XX Human adipocyte complement related protein homologue zacrp3, SEQ ID NO:2.
DE
XX Human zacrp3; adipocyte complement related protein homologue;
KW

KW ACRP30; Clq domain; collagen-like domain; energy balance modulation;
KW cellular metabolism; metabolic disorder; obesity; anorexia;
KW antimicrobial agent; infection; platelet aggregation inhibition;
KW adhesion; activation; vascular injury; antibacterial; antiviral.
XX
OS Homo sapiens.
XX
PN WO200063377-A1.
XX
XX 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10454.
XX
PR 20-APR-1999; 99US-0294943.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Piddington CS, Bishop PD;
XX WPI; 2000-665243/64.
XX N-PSDB; AAC64058.
XX
PT Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
PT infections, for wound healing, improving blood flow, and to analyze
PT energy efficiency in mammals -
XX
PS Claim 2; Page 109-110; 123pp; English.

CC The invention relates to the human zacrp3 protein (AAB29580) and to
CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homologue
CC of adipocyte complement related protein (ACRP30) and contains a
CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC C-terminal Clq domain comprising 10 beta-strands. The zacrp3 gene is
CC located on chromosome 5p12. The invention also relates to zacrp3
CC fragments, fusion proteins containing zacrp3 polypeptides,
CC zacrp3-specific antibodies, expression constructs and host cells
CC comprising zacrp3 nucleic acids, and methods of recombinant production of
CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
CC study and modulation of cellular metabolism and energy balance in
CC mammals, and may therefore be used to treat disorders such as obesity and
CC anorexia, and conditions associated with these disorders. Due to its Clq
CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
CC as antimicrobial agents, promoting lysis or phagocytosis of infectious
CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
CC proteins, antibodies and activity modulators may also be used to inhibit
CC collagen-induced platelet aggregation, adhesion, or activation, and may
CC therefore have potential for promoting blood flow within the vasculature
CC of a mammal e.g., to treat injury to the vasculature or other collagenous
CC tissue. Human zacrp3 and its antibodies may additionally be used to study
CC dimerisation and oligomerisation. The present sequence represents human
CC zacrp3.

Sequence 246 AA;
Query Match 100.0%; Score 1367; DB 21; Length 246;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWRQLIYWQLLALFFLPCLCODEYMESFQTGLPPDCSKCHGYSFRGYGPPGPG 60
DB 1 MLWRQLIYWQLLALFFLPCLCODEYMESFQTGLPPDCSKCHGYSFRGYGPPGPG 60
QY 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120
DB 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120
QY 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRGAPVSGVYFFTFMSMKHEDVEEYV 180
DB 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRGAPVSGVYFFTFMSMKHEDVEEYV 180
QY 181 YLMHNGNTVFSMYSYEMKKGSDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRFSFAGF 240
DB 181 YLMHNGNTVFSMYSYEMKKGSDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRFSFAGF 240

QY 241 LLFETK 246
Db 241 LLFETK 246
RESULT 3
AAB18909
ID AAB18909 standard; Protein; 246 AA.
AC AAB18909;
XX
XX 08-FEB-2001 (first entry)
DE A novel polypeptide designated PRO1484.
XX
KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW insulinemia; kidney disorder; Bergers disease; nephropathy;
KW Schonlein-Henoch purpura; celliac disease; dermatitis herpeticiformis;
KW Crohns disease.
XX
XX Homo sapiens.
XX
XX
FH Location/Qualifiers
FT Peptide
FT 1..22
FT /note= "signal peptide"
FT Domain
FT 33..66
FT /note= "Clq domain protein"
FT Domain
FT 42..75
FT /note= "Clq domain protein"
FT Domain
FT 45..78
FT /note= "Clq domain protein"
FT Domain
FT 48..81
FT /note= "Clq domain protein"
FT Domain
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FT 66..99
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FT /note= "Clq domain protein"
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FT 202..221
FT /note= "Clq domain protein"
FT Domain
FT 235..244
FT /note= "Clq domain protein"
XX WO200056889-A2.
XX
XX 28-SEP-2000.
XX
XX
XX 01-MAR-2000; 2000WO-US05601.
XX
XX 23-MAR-1999; 99US-0125774.
XX 23-MAR-1999; 99US-0125778.
PR 23-MAR-1999; 99US-0125826.
PR 31-MAR-1999; 99US-0127035.
PR 05-APR-1999; 99US-0127706.
PR 21-APR-1999; 99US-0130359.
PR 27-APR-1999; 99US-0131270.

PR 27-APR-1999; 99US-0131272.
PR 27-APR-1999; 99US-0131291.
PR 04-MAY-1999; 99US-0132371.
PR 04-MAY-1999; 99US-0132379.
PR 04-MAY-1999; 99US-0132383.
PR 25-MAY-1999; 99US-0135750.
PR 08-JUN-1999; 99US-0138166.
PR 20-JUL-1999; 99US-0144791.
PR 03-AUG-1999; 99US-0146970.
PR 09-DEC-1999; 99US-0170262.
XX
XX (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2000-628263/60.
DR N-PSDB; AAA96336.
XX
XX Novel secreted and transmembrane polypeptides useful for diagnosing
PT tumour in a mammal, for identifying agonists and antagonists of the
PT polypeptide and for therapeutic use -
XX
XX Claim 12; Fig 2; 222pp; English.
XX
XX The present sequence represents a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499, PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells
CC and are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celliac disease,
CC dermatitis herpeticiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing.
XX
SQ Sequence 246 AA;
Query Match 100.0%; Score 1367; DB 21; Length 246;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPTGGLPDCSKCCGHDYSFRGYQGPPGPG 60
Db 1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPTGGLPDCSKCCGHDYSFRGYQGPPGPG 60
Qy 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYGPIPPQLQIAF 120
Db 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYGPIPPQLQIAF 120
Qy 121 MASLATHSNQNSGIIFSSVETNIGNFDDVMTGRFAPVSGVYFFTFSMKHEDVEEYV 180
Db 121 MASLATHSNQNSGIIFSSVETNIGNFDDVMTGRFAPVSGVYFFTFSMKHEDVEEYV 180
Qy 181 YLMHNGNTVFSWYSEYEMKGS DTSNHA VLKLAGDVEWLRMGALHGHDHQRSTFAGF 240
Db 181 YLMHNGNTVFSWYSEYEMKGS DTSNHA VLKLAGDVEWLRMGALHGHDHQRSTFAGF 240
Qy 241 LLFETK 246
Db 241 LLFETK 246
RESULT 4
AAB88447
ID AAB88447 standard; Protein; 246 AA.

XX AAB88447;
 AC 23-MAY-2001 (first entry)
 DT Human membrane or secretory protein clone PSEC0232.
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;
 XX rheumatoid arthritis; diabetes.
 KW Homo sapiens.
 OS EP1067182-A2.
 XX 10-JAN-2001.
 PN 07-JUL-2000; 2000EP-0114090.
 XX 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 XX 02-MAY-2000; 2000JP-0183766.
 XX (HELI-) HELIX RES INST.
 PA Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 PI WPI; 2001-093989/11.
 XX N-PSDB; AAF93874.
 DR Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 XX Claim 1: SEQ ID 262; 609pp + CD ROM; English.
 PS This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretion and
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid
 CC arthritis and diabetes.
 XX Sequence 246 AA;
 SQ Query Match 100.0%; Score 1367; DB 22; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2e-124;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWRQLIYWQLLALFPLPCLQDEYMESPTQGLPPDCSKCHGDYSRPGYGGPPPG 60
 DB 1 MLWRQLIYWQLLALFPLPCLQDEYMESPTQGLPPDCSKCHGDYSRPGYGGPPPG 60
 QY 61 PPGIPGNHNNNGATGHEGAKGKGDGLPRGGRGQHGPKGKGYGPPPELQIAF 120
 DB 61 PPGIPGNHNNNGATGHEGAKGKGDGLPRGGRGQHGPKGKGYGPPPELQIAF 120

QY 121 MASLATHFSNQSGIIFSSVETNIGNFFDMTGRFCAPYSGVYFFTFSMKKHEDVEVYV 180
 DB 121 MASLATHFSNQSGIIFSSVETNIGNFFDMTGRFCAPYSGVYFFTFSMKKHEDVEVYV 180
 QY 181 YLMHNGNTVFSMYSEYEMKCKSDTSSNHAVLKLAAGDEVWLRMGNGALHGDFSTFAGF 240
 DB 181 YLMHNGNTVFSMYSEYEMKCKSDTSSNHAVLKLAAGDEVWLRMGNGALHGDFSTFAGF 240
 QY 241 LLFETK 246
 DB 241 LLFETK 246
 RESULT 5
 AAU84371
 ID AAU84371 standard; Protein; 246 AA.
 XX AC AAU84371;
 XX DT 08-MAY-2002 (first entry)
 XX DE Novel human secreted or membrane-associated protein #10.
 XX KW Human; secreted protein; membrane-associated protein; hypertension;
 KW inflammatory disorder; neurological disorder; haematopoietic disorder;
 KW skeletal developmental disorder; growth abnormality; autoimmune disorder;
 KW neurodegenerative disorder; nervous system disorder; bacterial infection;
 KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
 KW hypotension; sexual development disorder; blood disorder.
 XX OS Homo sapiens.
 XX PN WO200204600-A2.
 PD 17-JAN-2002.
 XX PF 12-JUL-2001; 2001WO-US21985.
 XX PR 12-JUL-2000; 2000US-218033P.
 XX PR 21-AUG-2000; 2000US-226517P.
 XX PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX PA (GLAX) GLAXO GROUP LTD.
 PI Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
 PI Smith RF, Xiang Z, Xie Q;
 XX WPI; 2002-188468/24.
 DR N-PSDB; ABK35591.
 XX Novel secreted and membrane-associated polypeptides and polynucleotides
 PT encoding the polypeptides, for preventing, treating and ameliorating
 PT cancers, mental or sexual developmental disorders, and malignant tumours
 PS Claim 1; Page 131-132; 151pp; English.
 CC The present invention relates to the isolation of novel human secreted
 CC or membrane-associated proteins and the genes encoding them. The
 CC sequences of the invention are useful for treating, preventing and
 CC ameliorating various diseases such as inflammatory disorders (e.g.
 CC asthma), neurological disorders (e.g. dementia), haematopoietic
 CC disorders, skeletal developmental disorders, growth abnormalities,
 CC neurodegenerative disorders (e.g. Huntington's disease), nervous system
 CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),
 CC peripheral myelinopathies, viral and bacterial infections,
 CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
 CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,
 CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental
 CC or sexual development disorders, and dysfunctions of the blood cascade
 CC system including those leading to stroke. AAU84362-AAU84389 represent
 CC the novel human secreted or membrane-associated proteins of the

```
CC invention.
XX
SQ Sequence 246 AA;
Query Match 100.0%; Score 1367; DB 23; Length 246;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWRQLIYWQLLALFFLPFCLODEYMEPOTGLPPDCSKCHGDSFRGYQGPYPGG 60
DB 1 MLWRQLIYWQLLALFFLPFCLODEYMEPOTGLPPDCSKCHGDSFRGYQGPYPGG 60
QY 61 PPGIPGNHNGNNGATGHEGAKGDKDGLGPRGGRGQHGKGEKGYGIPPELQIAF 120
DB 61 PPGIPGNHNGNNGATGHEGAKGDKDGLGPRGGRGQHGKGEKGYGIPPELQIAF 120
QY 121 MASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFPVSGVGYFFTFSSMKKHEDVEEYV 180
DB 121 MASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFPVSGVGYFFTFSSMKKHEDVEEYV 180
QY 181 YLMINGNTVFSMYSEMKGKSDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRSTFAGF 240
DB 181 YLMINGNTVFSMYSEMKGKSDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRSTFAGF 240
QY 241 LLEFETK 246
DB 241 LLEFETK 246
RESULT 6
AAU84370
ID AAU84370 standard; Protein: 319 AA.
XX
AC AAU84370;
XX
DT 08-MAY-2002 (first entry)
XX
DE Novel human secreted or membrane-associated protein #9.
XX
KW Human; secreted protein; membrane-associated protein; hypertension;
KW inflammatory disorder; neurological disorder; haematopoietic disorder;
KW skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW neurodegenerative disorder; nervous system disorder; bacterial infection;
KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW hypotension; sexual development disorder; blood disorder.
XX
OS Homo sapiens.
XX
PN WO200204600-A2.
XX
PD 17-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-US21985.
XX
PR 12-JUL-2000; 2000US-218033P.
XX
PR 21-AUG-2000; 2000US-226517P.
XX
PA (SMK ) SMITHKLINE BEECHAM CORP.
PA (SMK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
XX
XX Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
PI Smith RF, Xiang Z, Xie Q;
XX WPI; 2002-188468/24.
XX DR N-PSDB; ABK35590.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT encoding the polypeptides, for preventing, treating and ameliorating
PT cancers, mental or sexual developmental disorders, and malignant tumours
XX
PS Claim 1; Page 130-131; 151pp; English.
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XX
CC The present invention relates to the isolation of novel human secreted
CC or membrane-associated proteins and the genes encoding them. The
CC sequences of the invention are useful for treating, preventing and
CC ameliorating various diseases such as inflammatory disorders (e.g.
CC asthma), neurological disorders (e.g. dementia), haematopoietic
CC disorders, skeletal developmental disorders, growth abnormalities,
CC neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC peripheral myelinopathies, viral and bacterial infections,
CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC or sexual development disorders, and dysfunctions of the blood cascade
CC system including those leading to stroke. AAU84362-AAU84389 represent
CC the novel human secreted or membrane-associated proteins of the
CC invention.
XX
SQ Sequence 319 AA;
Query Match 96.6%; Score 1320.5; DB 23; Length 319;
Best Local Similarity 77.1%; Pred. No. 9.3e-120;
Matches 246; Conservative 0; Mismatches 0; Indels 73; Gaps 1;
QY 1 MLWRQLIYWQLLALFFLPFCLODEYME----- 28
DB 1 MLWRQLIYWQLLALFFLPFCLODEYMEVSGRTNKVARIVOSHQQTGRSSRREKVRER 60
QY 29 -----SPQTGGLPPDCSKCHG 47
DB 61 SHPKTGTVDNNTSTDLSLRPDELPHPEVDLLAQITTFWGOSPTGGLPPDCSKCHG 120
QY 48 SFRGYQGPYPGGIPGNHNGNNGATGHEGAKGDKDGLGPRGGRGQHGKGEK 107
DB 121 SFRGYQGPYPGGIPGNHNGNNGATGHEGAKGDKDGLGPRGGRGQHGKGEK 180
QY 108 GYPGIPPELQIAFASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFPVSGVGYFFTF 167
DB 181 GYPGIPPELQIAFASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFPVSGVGYFFTF 240
QY 168 SMKHEDVEEYVYLMHNGNTVFSMYSEMKGKSDTSSNHAVALKLAKGDEVWLRMGNGAL 227
DB 241 SMKHEDVEEYVYLMHNGNTVFSMYSEMKGKSDTSSNHAVALKLAKGDEVWLRMGNGAL 300
QY 228 HGDHQRSTFAGFLLEFETK 246
DB 301 HGDHQRSTFAGFLLEFETK 319
RESULT 7
AAB29582
ID AAB29582 standard; Protein: 246 AA.
XX
AC AAB29582;
XX
DT 19-FEB-2001 (first entry)
XX
DE Mouse zacr2 protein, SEQ ID NO:12.
KW Mouse zacr2; adipocyte complement related protein homologue;
KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW cellular metabolism; metabolic disorder; obesity; anorexia;
KW antimicrobial agent; infection; platelet aggregation inhibition;
KW adhesion; activation; vascular injury; antibacterial; antiviral;
XX human zacr3 homologue.
XX
OS Mus musculus.
XX
PN WO2000063377-A1.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10454.
```

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XX 20-APR-1999; 99US-0294943.
XX (ZYMO ) ZYMOGENETICS INC.
XX Piddington CS, Bishop PD;
XX WPI; 2000-665243/64.
XX N-PSDB; AAC64064.
XX Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
XX infections, for wound healing, improving blood flow, and to analyze
XX energy efficiency in mammals -
XX Disclosure; Page 117-118; 123pp; English.
XX The invention relates to the human zacrp3 protein (AAB29580) and to
XX nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homologue
XX of adipocyte complement related protein (ACRP30) and contains a
XX collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
XX C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is
XX located on chromosome 5p12. The invention also relates to zacrp3
XX fragments, fusion proteins containing zacrp3 polypeptides,
XX zacrp3-specific antibodies, expression constructs and host cells
XX comprising zacrp3 nucleic acids, and methods of recombinant production of
XX zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
XX study and modulation of cellular metabolism and energy balance in
XX mammals, and may therefore be used to treat disorders such as obesity and
XX anorexia, and conditions associated with these disorders. Due to its C1q
XX like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
XX as antimicrobial agents, promoting lysis or phagocytosis of infectious
XX organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
XX proteins, antibodies and activity modulators may also be used to inhibit
XX collagen-induced platelet aggregation, adhesion, or activation, and may
XX therefore have potential for promoting blood flow within the vasculature
XX of a mammal e.g., to treat injury to the vasculature or other collagenous
XX tissue. Human zacrp3 and its antibodies may additionally be used to study
XX dimerisation and oligomerisation. The present sequence represents mouse
XX zacrp2, a homologue of human zacrp3.
XX Sequence 246 AA;
XX Query Match 95.9%; Score 1311; DB 21; Length 246;
XX Best Local Similarity 95.9%; Pred. NO. 5.5e-119;
XX Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 MLNRQLIYWQLLALFLPFLCQDEYNESQGTGLPPDCSKCHGDSYRFGYQGPFGPG 60
Db 1 MLGRQRIWHLLPFLPFLCQDEYNESQAGGLPPDCSKCHGDSYRFGYQGPFGPG 60
QY 61 PPGIPGNHGNNGNATGHEGAKGKGDGLGPRGERGHGPKGKGYPIPELQIAF 120
Db 61 PPGIPGNHGNNGNATGHEGAKGKGDGLGPRGERGHGPKGKGYPIPELQIAF 120
QY 121 MASLATHFSNQNGIIFSSVETNIGNFDMVTGRFGAPVSGVYFFTFSMKKHEDVEEYV 180
Db 121 MASLATHFSNQNGIIFSSVETNIGNFDMVTGRFGAPVSGVYFFTFSMKKHEDVEEYV 180
QY 181 YLMHNGNTVFSMYSYEMKGSQDTSNHAHLKLAKGDEVWLRMGNGALHGDHQRFFSTFAGF 240
Db 181 YLMHNGNTVFSMYSYETKGSQDTSNHAHLKLAKGDEVWLRMGNGALHGDHQRFFSTFAGF 240
QY 241 LLFETK 246
Db 241 LLFETK 246
RESULT 8
AAM99925
ID AAM99925 standard; Protein; 225 AA.
XX
AC AAM99925;
XX
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DT 07-JAN-2002 (first entry)
XX Human polypeptide SEQ ID NO 41.
DE
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200155173-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01356.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-020515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR	14-SEP-2000;	2000US-02324000;	2000US-02324000;
PR	14-SEP-2000;	2000US-02324013;	2000US-02324013;
PR	14-SEP-2000;	2000US-02324061;	2000US-02324061;
PR	14-SEP-2000;	2000US-02323064;	2000US-02323064;
PR	14-SEP-2000;	2000US-02323065;	2000US-02323065;
PR	21-SEP-2000;	2000US-02342233;	2000US-02342233;
PR	21-SEP-2000;	2000US-02342274;	2000US-02342274;
PR	25-SEP-2000;	2000US-02349977;	2000US-02349977;
PR	25-SEP-2000;	2000US-02349988;	2000US-02349988;
PR	26-SEP-2000;	2000US-02354884;	2000US-02354884;
PR	27-SEP-2000;	2000US-02358634;	2000US-02358634;
PR	27-SEP-2000;	2000US-02358636;	2000US-02358636;
PR	29-SEP-2000;	2000US-02363277;	2000US-02363277;
PR	29-SEP-2000;	2000US-02363677;	2000US-02363677;
PR	29-SEP-2000;	2000US-02363688;	2000US-02363688;
PR	29-SEP-2000;	2000US-02363699;	2000US-02363699;
PR	29-SEP-2000;	2000US-02363730;	2000US-02363730;
PR	02-OCT-2000;	2000US-02368602;	2000US-02368602;
PR	02-OCT-2000;	2000US-02370733;	2000US-02370733;
PR	02-OCT-2000;	2000US-02370739;	2000US-02370739;
PR	02-OCT-2000;	2000US-02370400;	2000US-02370400;
PR	13-OCT-2000;	2000US-02399935;	2000US-02399935;
PR	13-OCT-2000;	2000US-02399937;	2000US-02399937;
PR	20-OCT-2000;	2000US-02409600;	2000US-02409600;
PR	20-OCT-2000;	2000US-02411221;	2000US-02411221;
PR	20-OCT-2000;	2000US-02417855;	2000US-02417855;
PR	20-OCT-2000;	2000US-02417865;	2000US-02417865;
PR	20-OCT-2000;	2000US-02417877;	2000US-02417877;
PR	20-OCT-2000;	2000US-02418008;	2000US-02418008;
PR	20-OCT-2000;	2000US-02418009;	2000US-02418009;
PR	20-OCT-2000;	2000US-02418266;	2000US-02418266;
PR	01-NOV-2000;	2000US-02461677;	2000US-02461677;
PR	08-NOV-2000;	2000US-02464774;	2000US-02464774;
PR	08-NOV-2000;	2000US-02464775;	2000US-02464775;
PR	08-NOV-2000;	2000US-02464776;	2000US-02464776;
PR	08-NOV-2000;	2000US-02464778;	2000US-02464778;
PR	08-NOV-2000;	2000US-02464780;	2000US-02464780;
PR	08-NOV-2000;	2000US-02464781;	2000US-02464781;
PR	08-NOV-2000;	2000US-02465223;	2000US-02465223;
PR	08-NOV-2000;	2000US-02465243;	2000US-02465243;
PR	08-NOV-2000;	2000US-02465255;	2000US-02465255;
PR	08-NOV-2000;	2000US-02465277;	2000US-02465277;
PR	08-NOV-2000;	2000US-02465278;	2000US-02465278;
PR	08-NOV-2000;	2000US-02465282;	2000US-02465282;
PR	08-NOV-2000;	2000US-02465609;	2000US-02465609;
PR	08-NOV-2000;	2000US-02466110;	2000US-02466110;
PR	08-NOV-2000;	2000US-02466113;	2000US-02466113;
PR	17-NOV-2000;	2000US-02492077;	2000US-02492077;
PR	17-NOV-2000;	2000US-02492080;	2000US-02492080;
PR	17-NOV-2000;	2000US-02492090;	2000US-02492090;
PR	17-NOV-2000;	2000US-02492110;	2000US-02492110;
PR	17-NOV-2000;	2000US-02492120;	2000US-02492120;
PR	17-NOV-2000;	2000US-02492122;	2000US-02492122;
PR	17-NOV-2000;	2000US-02492114;	2000US-02492114;
PR	17-NOV-2000;	2000US-02492116;	2000US-02492116;
PR	17-NOV-2000;	2000US-02492117;	2000US-02492117;
PR	17-NOV-2000;	2000US-02492129;	2000US-02492129;
PR	17-NOV-2000;	2000US-02492944;	2000US-02492944;
PR	17-NOV-2000;	2000US-02492945;	2000US-02492945;
PR	17-NOV-2000;	2000US-02492965;	2000US-02492965;
PR	17-NOV-2000;	2000US-02492967;	2000US-02492967;
PR	17-NOV-2000;	2000US-02492977;	2000US-02492977;
PR	17-NOV-2000;	2000US-02493000;	2000US-02493000;
PR	01-DEC-2000;	2000US-02501160;	2000US-02501160;
PR	01-DEC-2000;	2000US-02503591;	2000US-02503591;
PR	05-DEC-2000;	2000US-02	

PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI; 2001-451924/48.	
DR	N-PSDB; AA199523.	
XX		
PT	New nucleic acids and polypeptides, useful for treating, preventing or ameliorating human disorders and diseases -	
PT		
XX		
PS	Claim 11; SEQ ID NO 41; 465pp + Sequence Listing; English.	
XX		
CC	The invention relates to novel human polynucleotides (AA199513-AA199530) and the encoded proteins (AAW9915-AAW9934) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues or disclosed in the specification. The nucleic acids, proteins, antibodies and (antagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.	
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
XX		
SQ	Sequence 225 AA;	
	Query Match 88.4%; Score 1208; DB 22; Length 225;	
	Best Local Similarity 99.5%; Pred. No. 4.9e-109;	
	Matches 218; Conservative 1; Mismatches 0; Indels 0; Gaps	
Qy	28 ESPQTGGIPLPDCSCCHGDISFRGYQGPPGPDPGPGIPGNHGNNNGATGHEGAKGEK 87	
Db	:	
	7 QSPQTGGIPLPDCSCCHGDISFRGYQGPPGPDPGPGIPGNHGNNNGATGHEGAKGEK 66	
Qy	88 DKGLDGRGRGQHGPKEKGYPGIPPELOIAFNASLATHFSNONGSIIFSSVETNIGNF 147	
Db	:	
	67 DKGLDGRGRGQHGPKEKGYPGIPPELOIAFNASLATHFSNONGSIIFSSVETNIGNF 126	
Qy	148 FDMVTGRGAPVSGYVFYFTFSMKKHEDVEEYVYLHMGNTVFSMYENMKGSDTSSNH 207	
Db	:	
	127 FDMVTGRGAPVSGYVFYFTFSMKKHEDVEEYVYLHMGNTVFSMYENMKGSDTSSNH 186	
Qy	208 AVLKLAKGDEVLRMNGALHGDHQRFSTFAGFLLFETK 246	
Db	:	
	187 AVLKLAKGDEVLRMNGALHGDHQRFSTFAGFLLFETK 225	
RESULT 9		
AAM41860		
ID	AAH41860 standard; Protein; 202 AA.	
XX		
AC	AAH41860;	
XX		
DT	22-OCT-2001 (first entry)	
XX		
DE	Human polypeptide SEQ ID NO 6791.	
XX		

SQ Sequence 223 AA;
Query Match 58.08; Score 792.5; DB 22; Length 223;
Best Local Similarity 66.86; Pred. No. 1e-68;
Matches 147; Conservative 0; Mismatches 0; Indels 73; Gaps 1;
QY 1 MLWRLIYWQLLALFFLPFCICQDEYME-----SPQTGGGLPPDCSKCCHGDY 28
DB 1 MLWRLIYWQLLALFFLPFCICQDEYMEVSGRTNKVARIYVQSHQQTGRSGSRREKVRER 60
QY 29 -----SPQTGGGLPPDCSKCCHGDY 47
DB 61 SHPKTGTVDNNTSLKSLRDELPHPEVDLQITTFWQSPQTGGGLPPDCSKCCHGDY 120
QY 48 SFRGYQGGPPGPPGIPGNGHNGNNGCATGHEGAKGKDGKDLGPRGERGQHGPKGK 107
DB 121 SFRGYQGGPPGPPGIPGNGHNGNNGCATGHEGAKGKDGKDLGPRGERGQHGPKGK 180
QY 108 GYPGIPPELQIAFASLATHESNONGIIFSSVETNIGNF 147
DB 181 GYPGIPPELQIAFASLATHESNONGIIFSSVETNIGNF 220
RESULT 11
AAY11485
ID AAY11485 standard; Protein: 128 AA.
XX AC AAY11485;
XX DT 21-JUN-1999 (first entry)
XX DE Human 5' EST secreted protein SEQ ID NO 307.
XX KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX KW forensic; gene therapy; chromosome mapping; signal peptide;
XX KW upstream regulatory sequence; cytokine activity; cell proliferation;
XX KW differentiation; haematopoiesis regulation; tissue growth regulation;
XX KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX KW thrombolytic; anti-inflammatory; tumour inhibition.
XX OS Homo sapiens.
XX PN WO9906551-A2.
XX PD 11-FEB-1999.
XX PF 31-JUL-1998; 98WO-IB01235.
XX PR 01-AUG-1997; 97US-0905133.
XX PA (GEST) GENSET.
XX PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX DR WPI: 1999-153781/13.
XX DR N-PSDB: AAX39551.
XX PT New nucleic acids encoding human secreted - proteins obtained from
XX PT cDNA libraries prepared from substantia nigra, cerebellum, surrenals
XX PT and fetal brain tissue
XX PS Claim 34; Page 402-403; 434pp; English.
XX CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
XX CC human secreted proteins, and encode the proteins given in AAY11374 to
XX CC AAY11531, respectively. The proteins given represent the signal peptide
XX CC and an N-terminal fragment of a secreted protein. The nucleic acid
XX CC sequences can be used for producing secreted human gene products. The
XX CC can also be used to develop products for diagnosis and therapy. The
XX CC proteins obtained may have cytokine activity, cell
XX CC proliferation/differentiation activity, haematopoiesis regulating
XX CC activity, tissue growth regulating activity, reproductive hormone
XX CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and

CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell.
XX SQ Sequence 128 AA;
Query Match 52.7%; Score 721; DB 20; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.2e-62;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWRLIYWQLLALFFLPFCICQDEYMESPTGGGLPPDCSKCCHGDYSFRGYQGGPPG 60
DB 1 MLWRLIYWQLLALFFLPFCICQDEYMESPTGGGLPPDCSKCCHGDYSFRGYQGGPPG 60
QY 61 PPGIPGNGHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYGIPPELQIAF 120
DB 61 PPGIPGNGHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYGIPPELQIAF 120
QY 121 MASL 124
DB 121 MASL 124
RESULT 12
AAM40074
ID AAM40074 standard; Protein: 126 AA.
XX AC AAM40074;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 3219.
XX KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX KW leukaemia.
XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao Qa, Zhou P, Goodrich R, Drmanac RT;
XX DR WPI: 2001-442253/47.
XX DR N-PSDB: AAI59230.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -

Example 5; SEQ ID NO 3219; 10078pp; English.

PS The invention relates to human nucleic acids (AAI57798-AAI61369) and
 XX the encoded polypeptides (AAI38642-AAI42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-brager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX SQ Sequence 126 AA;

Query Match 48.5%; Score 663; DB 22; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.8e-56;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 MASLATHFSNQSGIIIFSSVETNIGNFVDYMTGRFGAPVSGVYFFTFSMKHEDVEYV 180
 DB 1 MASLATHFSNQSGIIIFSSVETNIGNFVDYMTGRFGAPVSGVYFFTFSMKHEDVEYV 60
 QY 181 YLMHNGNTVFSMYEMKGSQDTSNNHAVLKLAKGDEVLRMNGALHGDRFSTFAGF 240
 DB 61 YLMHNGNTVFSMYEMKGSQDTSNNHAVLKLAKGDEVLRMNGALHGDRFSTFAGF 120
 QY 241 LLFETK 246
 DB 121 LLFETK 126

RESULT 13

AAV75969
 ID AAY75969 standard; Protein; 105 AA.

XX AAY75969;

XX 27-MAR-2000 (first entry)

XX Rat skin cell protein, SEQ ID 147.

XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery.

XX Rattus sp.

OS WO9955865-A1.

XX 04-NOV-1999.

XX 29-APR-1999; 99WO-NZ00051.

XX 29-APR-1998; 98US-0069726.

XX 09-NOV-1998; 98US-0188930.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
 PI WPI; 2000-072177/06.

XX Novel polynucleotides useful for the treatment of various conditions

PT including wounds and cancer -

XX Claim 4; Page 112-113; 235pp; English.

XX The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
 CC by cDNA sequences derived from several mouse, rat or human skin cell
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
 CC putative transmembrane domains.

XX SQ Sequence 105 AA;

Query Match 42.6%; Score 582; DB 21; Length 105;
 Best Local Similarity 93.3%; Pred. No. 1e-48;
 Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLWRQLIYWOLLALFLPFCLODEYMESQGTGLPPDCSKCHGYSFRGYGPPGPG 60

DB 1 MLRRQLVWHLALLFLPFCLODEYMESQAGGLPPDCSKCHGYSFRGYGPPGPG 60

QY 61 PPGIPGNHNGNNGATGHEGAKGEKDGKDLGPRGERGHPKG 105

DB 61 PPGIPGNHNGNNGATGHEGAKGEKDGKDLGPRGERGHPKG 105

RESULT 14

AAV76025
 ID AAY76025 standard; Protein; 105 AA.

XX AAY76025;

XX 27-MAR-2000 (first entry)

XX Rat skin cell protein, SEQ ID NO:280.

XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery.

XX Rattus sp.

OS WO9955865-A1.

XX 04-NOV-1999.

XX 29-APR-1999; 99WO-NZ00051.

XX 29-APR-1998; 98US-0069726.

XX 09-NOV-1998; 98US-0188930.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
 PI WPI; 2000-072177/06.

XX N-PSDB; AAZ61730.

XX Novel polynucleotides useful for the treatment of various conditions

PT including wounds and cancer -

PS Claim 4; Page 168; 235pp; English.

XX The invention relates to novel nucleic acid sequences derived from rat
CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC cells. Polypeptides of the invention may be used to treat inflammation,
CC cancer and neurological diseases. The proteins may be used to stimulate
CC the growth and motility of keratinocytes, to inhibit the growth of
CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC modulate skin inflammation, to modulate epithelial cell growth and to
CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC to treat growth and developmental defects, skin wounds and hair follicle
CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
CC by cDNA sequences derived from several mouse, rat or human skin cell
CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
CC AAY76119 are proteins with an N-terminal signal sequence, indicating
CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
CC putative transmembrane domains.

XX Sequence 105 AA;

Query Match 42.6%; Score 582; DB 21; Length 105;

Best Local Similarity 93.3%; Pred. No. 1e-48;

Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLWRQLIYWQLLALFFLPFCQDEYMESPTQGGLPDCCSKCHGDYSGRGYQGGPPPG 60

DB 1 MLRRQLVVMHLLALLFLPFCQDEYMESPTQAGGLPPDCCSKCHGDYSGRGYQGGPPPG 60

QY 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

DB 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

RESULT 15

AAB55908

ID AAB55908 standard; Protein; 105 AA.

XX AAB55908;

AC AAB55908;

DT 08-MAR-2001 (first entry)

DE Skin cell protein, SEQ ID NO: 147.

XX Rat; skin cell; cytostatic; anti-inflammatory; anti-HIV;

KW neutropic; neuroprotective; vulnary; immunomodulatory; vaccine;

KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;

XX inflammation; neurological disease.

OS Rattus sp.

XX WO200069884-A2.

PN 23-NOV-2000.

XX 15-MAY-2000; 2000WO-NZ00075.

XX 14-MAY-1999; 99US-0312283.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

DR WPI; 2001-007495/01.

XX N-PSDB; AAC99566, AAC99776.

PT New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -

XX

PS Claim 4; Page 147; 352pp; English.

XX The present sequence is a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.

SQ Sequence 105 AA;

Query Match 42.6%; Score 582; DB 22; Length 105;

Best Local Similarity 93.3%; Pred. No. 1e-48;

Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLWRQLIYWQLLALFFLPFCQDEYMESPTQGGLPDCCSKCHGDYSGRGYQGGPPPG 60

DB 1 MLRRQLVVMHLLALLFLPFCQDEYMESPTQAGGLPPDCCSKCHGDYSGRGYQGGPPPG 60

QY 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

DB 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

Search completed: January 13, 2003, 10:42:49

Job time : 38 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:42:48 ; Search time 15 Seconds
(without alignments)
482.536 Million cell updates/sec

Title: US-09-931-836-2
Perfect score: 1367
Sequence: 1 MLWRQLIYWOLLALFLPFC.....LHGDHQRFSTFAGFLPETK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pap.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	42.6	105	US-09-188-930-147	Sequence 147, App
2	582	42.6	105	US-09-188-930-280	Sequence 280, App
3	316	23.1	294	US-09-188-930-294	Sequence 294, App
4	294	21.5	247	US-08-463-911-2	Sequence 2, Appl
5	293.5	21.5	231	US-09-530-423-2	Sequence 2, Appl
6	293.5	21.5	244	US-08-463-911-7	Sequence 7, Appl
7	293.5	21.5	244	US-09-140-804-3	Sequence 3, Appl
8	293.5	21.5	244	US-09-336-536-20	Sequence 20, Appl
9	287	21.0	247	US-09-530-423-1	Sequence 1, Appl
10	287	21.0	247	US-09-140-804-8	Sequence 8, Appl
11	287	21.0	247	US-09-118-408-3	Sequence 3, Appl
12	287	21.0	247	US-09-506-855-3	Sequence 3, Appl
13	274	20.0	246	US-08-463-911-4	Sequence 4, Appl
14	273	20.0	746	US-09-370-838-185	Sequence 185, App
15	264.5	19.3	228	US-09-336-536-4	Sequence 4, Appl
16	264.5	19.3	243	US-09-140-804-2	Sequence 2, Appl
17	264.5	19.3	243	US-09-336-536-3	Sequence 3, Appl
18	254.5	18.6	243	US-09-336-536-10	Sequence 10, Appl
19	252.5	18.5	228	US-09-336-536-11	Sequence 11, Appl
20	252.5	18.5	243	US-09-188-930-295	Sequence 295, App
21	237.5	17.4	281	US-09-118-408-44	Sequence 44, Appl
22	237.5	17.4	281	US-09-506-855-44	Sequence 44, Appl
23	226	16.5	281	US-09-118-408-2	Sequence 2, Appl
24	226	16.5	281	US-09-506-855-2	Sequence 2, Appl
25	226	16.5	423	US-08-383-744-2	Sequence 2, Appl
26	226	16.5	423	US-08-999-336-2	Sequence 2, Appl
27	226	16.5	423	PCT-US96-01427-2	Sequence 2, Appl

28	219	16.0	245	4	US-09-140-804-4	Sequence 4, Appl
29	202	14.8	215	4	US-09-140-804-5	Sequence 5, Appl
30	200.5	14.7	198	4	US-09-188-930-138	Sequence 138, App
31	196	14.3	222	4	US-09-140-804-7	Sequence 7, Appl
32	194	14.2	185	2	US-08-463-911-3	Sequence 3, Appl
33	192	14.0	623	4	US-09-029-348-3	Sequence 3, Appl
34	192	14.0	626	4	US-09-029-348-2	Sequence 2, Appl
35	186	13.6	236	4	US-09-140-804-6	Sequence 6, Appl
36	185	13.5	357	1	US-07-609-716-66	Sequence 66, Appl
37	185	13.5	357	1	US-08-642-255-33	Sequence 33, Appl
38	185	13.5	357	4	US-08-475-411A-66	Sequence 66, Appl
39	185	13.5	357	4	US-08-478-029A-66	Sequence 66, Appl
40	184.5	13.5	684	1	US-08-555-669-12	Sequence 12, Appl
41	184.5	13.5	684	3	US-09-073-663-12	Sequence 12, Appl
42	183.5	13.4	532	1	US-08-494-168-9	Sequence 9, Appl
43	183	13.4	489	2	US-08-794-795-7	Sequence 7, Appl
44	183	13.4	489	4	US-09-249-200-7	Sequence 7, Appl
45	183	13.4	518	1	US-08-392-367B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-188-930-147
; Sequence 147, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 147
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-147
Query Match 42.6%; Score 582; DB 4; Length 105;
Best Local Similarity 93.3%; Pred. No. 2.1e-51;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 MLWRQLIYWOLLALFLPFCLODEYMEPOTGGLPDCKCKCHGDSYFRGYQGPPGPG 60
Db 1 MLRRLVWHLALLFLPFCLODEYMEPOTGGLPDCKCKCHGDSYFRGYQGPPGPG 60
QY 61 PPGIFGNHNNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105
Db 61 PPGIFGNHNNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105
RESULT 2
US-09-188-930-280
; Sequence 280, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-280

Query Match 42.6%; Score 582; DB 4; Length 105;
Best Local Similarity 93.3%; Pred. No. 2.1e-51;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLWRQLYVWLLALFFLCQDEYMESPTGGLPPDCSKCHGYSFRGYQGPFGPPG 60

Db 1 MLRRQLVWHLALLFFLCQDEYMESPAAGLPPDCSKCHGYSFRGYQGPFGPPG 60

QY 61 PPGIPGNHGNNGNNGATGHEGAKGKGDGLGPRGERGQHGPKG 105

Db 61 PPGIPGNHGNNGNNGATGHEGAKGKGDGLGPRGERGQHGPKG 105

RESULT 3

US-09-188-930-294
; Sequence 294, Application US/09188930A
; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Mathew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 294

; LENGTH: 294

; TYPE: PRT

; ORGANISM: Rat

US-09-188-930-294

Query Match 23.1%; Score 316; DB 4; Length 294;

Best Local Similarity 28.9%; Pred. No. 5.7e-24;

Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;

QY 6 LIYWQLIALFFLPCLCQDEYM-----ESPQTGGLPPDCSKCHGYSFRGYQGPFGPP 59

Db 10 MISMWLLAC-ALP--CAADPMLGAFARRDFQKGPQLVCS-----LPGQGP 54

QY 60 GPPGIPGNHGNNGNNGATGHEGAKGKGD-----L 92

Db 55 GPPGAPGSSVMGRMFPKQDQGDQDGRDSDGEGPGRTNRRKQGPKGKAGAI 114

QY 93 GPRGER-----COHQPKGKGYGIP-----PELQIAFMASLATHFSNQNS 133

Db 115 GPRGPGVSTPKHGIPKKGKPKGKSAFSAVTKSYPRERL 174

QY 134 GIIFSSVETNIGNFFDMVTRFCGAPVSGVYFFTFSSM--KHEDEVVYVLMHNGT 190

Db 175 PIKFDKILNMEGHYVYVLMHNGT-----LAIGLVHNGQ--Y 227

QY 191 SMYSYEMK-GKSDTSSNHAVLKLAKEDEVWLRM-----GNGALHGDHQRSTFAGFL 243

Db 228 RIRTFDANTGNHDVAGSGSTILALKEDEVWLRMIFYSQNGFLFYDPYWTDSLTGFL 285

RESULT 4

US-08-463-911-2

; Sequence 2, Application US/08463911

; Patent No. 5869330
; GENERAL INFORMATION:
; APPLICANT: Scherer, Philipp E.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,911

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI95-05

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-463-911-2

Query Match 21.5%; Score 294; DB 2; Length 247;

Best Local Similarity 31.5%; Pred. No. 7.4e-22;

Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

QY 6 LIYWQLIALFFLPCLCQDEYMESPTG--LPPDCSKCHGYSFRGYQGPFGPPG 63

Db 2 LLLQALLFLILP-SHAEDDVTTTEELAPALVPPKGTCA-----GMA--GIPG 48

QY 64 IPNHNHNGNNGATGHEGAKGKGDGLGPRGER---GOHQPKGKGYGIPPE----- 115

Db 49 HPNGHTPGDRDGTGPKGKGDAGLLGPKGETGDMGTGAEGRPFPTGPKGEPG 108

QY 116 ----LQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDMVTRFCGAPVSGVYFFTFSSM 170

Db 109 EAYMTSRSAFSGLETRVTPNVPPIRFTKIFYNQNHYDGTGKFCYNIGLIFYFSHIT 168

QY 171 KHEDEVVYVLMHNGTNTVFSMYSYEMKSDTSSNHAVLKLAKEDEVWLRM-GNG--A 226

Db 169 VY--MKDVKVSLEFKDKAVLFTYDQYQKNDVQASGVLLHLEVQDVQVLYQVYGDG 226

QY 227 LHGDHQRSTFAGFLF 243

Db 227 LYADNVNDSTFTGFLY 243

RESULT 5

US-09-530-423-2

; Sequence 2, Application US/09530423

; Patent No. 6461821

; GENERAL INFORMATION:

; APPLICANT: Otsuka Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a

; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit

; TITLE OF INVENTION: therefor

; FILE REFERENCE: P98-51


```
; CURRENT APPLICATION NUMBER: US/09/530.423
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: JP H9-297569
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Abdominal fat tissue from myoma uteri
US-09-530-423-2

Query Match      21.5%; Score 293.5; DB 4; Length 231;
Best Local Similarity 34.5%; Pred. No. 7.6e-22;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

Qy 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKDGKGD---LGPR---GE 97
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 QGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGTGCGEKGKDPGLIGPKGDIGE 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 98 RGQHPKGEKGYPGI-----PPE-----LQIAFASLATHESNQNGLIIFSSVETNIGNF 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 TGVPGAEGPRGPGIQRKGEPEGAYVRSFVGLTYVTIPNMPIRFTKIFYNQNH 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 148 FDMVTGRFGAPVSGVYFFTFSMKHEDVEEYVYLMHNGNTVFSMYEMKGSKSDTSNNH 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 YDSTGKFHCNIPGLYFAHYITVY--MKDVKVSLEKDKKAMLFYDYQYQENNVDAQSGS 187
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 208 AVLKAGDEWLKRM-GNG-----ALHGDHQRFEFTAGFLFF 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-08-463-911-7
; Sequence 7, Application US/08463911
; Patent No. 5869330
; GENERAL INFORMATION:
; APPLICANT: Scherer, Philipp E.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: US/08/463,911
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI95-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-911-7
```

```
Query Match      21.5%; Score 293.5; DB 2; Length 244;
Best Local Similarity 34.5%; Pred. No. 8.2e-22;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

Qy 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKDGKGD---LGPR---GE 97
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGTGCGEKGKDPGLIGPKGDIGE 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 98 RGQHPKGEKGYPGI-----PPE-----LQIAFASLATHESNQNGLIIFSSVETNIGNF 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TGVPGAEGPRGPGIQRKGEPEGAYVRSFVGLTYVTIPNMPIRFTKIFYNQNH 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 148 FDMVTGRFGAPVSGVYFFTFSMKHEDVEEYVYLMHNGNTVFSMYEMKGSKSDTSNNH 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDSTGKFHCNIPGLYFAHYITVY--MKDVKVSLEKDKKAMLFYDYQYQENNVDAQSGS 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 208 AVLKAGDEWLKRM-GNG-----ALHGDHQRFEFTAGFLFF 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-09-140-804-3
; Sequence 3, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-804-3

Query Match      21.5%; Score 293.5; DB 4; Length 244;
Best Local Similarity 34.5%; Pred. No. 8.2e-22;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

Qy 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKDGKGD---LGPR---GE 97
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGTGCGEKGKDPGLIGPKGDIGE 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 98 RGQHPKGEKGYPGI-----PPE-----LQIAFASLATHESNQNGLIIFSSVETNIGNF 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TGVPGAEGPRGPGIQRKGEPEGAYVRSFVGLTYVTIPNMPIRFTKIFYNQNH 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 148 FDMVTGRFGAPVSGVYFFTFSMKHEDVEEYVYLMHNGNTVFSMYEMKGSKSDTSNNH 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDSTGKFHCNIPGLYFAHYITVY--MKDVKVSLEKDKKAMLFYDYQYQENNVDAQSGS 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 208 AVLKAGDEWLKRM-GNG-----ALHGDHQRFEFTAGFLFF 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-336-536-20
; Sequence 20, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, K.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
```


Db 2 LLLQALLFLILP-SHAEDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48
QY 64 IPGNHNGNNGATGHEGAKGKGDGLGPRGER--GQHPKPKGKGYG-----GIPP 114
Db 49 HPGHNGTGRDGRDGTGPKGKGDAGLLGPKGETGDVMTGAEGPRGFPQTPGRKGE 108
QY 115 E----LQIAFMASLATHFSNQSGIIFSSVEINIGNFFDVMGRGAPVSGVYFFTFMM 170
Db 109 EAAVMYRSFVSGLETRVTPVNPPIRTKIFYNQNHQHDGSGTKFCYNIPGLYFYSYHIT 168
QY 171 KHEDEVEVYVYLMHNGNTVFSMYSYEMKGSDDTSSNHAHLKAKGDEVWLRM-GNG---A 226
Db 169 VY--MKDVKVSFLFKDKAVLFTYDQYQKKNVDQAGSVLLHLEVGQVWLQVYGDGDHNG 226
QY 227 LHGDHOREFSTAGFLFLF 243
Db 227 LYADNVNDSTFTGFLLY 243

RESULT 12
US-09-506-855-3
; Sequence 3, Application US/09506855
; Patent No. 6448221
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Lasser, Gerald W.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
; FILE REFERENCE: 99-12
; CURRENT APPLICATION NUMBER: US/09/506.855
; FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-506-855-3

Query Match 21.08; Score 287; DB 4; Length 247;
Best Local Similarity 31.98; Pred. No. 3.8e-21;
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;
QY 6 LIYMOLLALFLPFCCLQDYMESPTGG--LPPDCSKCHGDSYFRGYQGPFGPPGPPG 63
Db 2 LLLQALLFLILP-SHAEDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48
QY 64 IPGNHNGNNGATGHEGAKGKGDGLGPRGER--GQHPKPKGKGYG-----GIPP 114
Db 49 HPGHNGTGRDGRDGTGPKGKGDAGLLGPKGETGDVMTGAEGPRGFPQTPGRKGE 108
QY 115 E----LQIAFMASLATHFSNQSGIIFSSVEINIGNFFDVMGRGAPVSGVYFFTFMM 170
Db 109 EAAVMYRSFVSGLETRVTPVNPPIRTKIFYNQNHQHDGSGTKFCYNIPGLYFYSYHIT 168
QY 171 KHEDEVEVYVYLMHNGNTVFSMYSYEMKGSDDTSSNHAHLKAKGDEVWLRM-GNG---A 226
Db 169 VY--MKDVKVSFLFKDKAVLFTYDQYQKKNVDQAGSVLLHLEVGQVWLQVYGDGDHNG 226
QY 227 LHGDHOREFSTAGFLFLF 243
Db 227 LYADNVNDSTFTGFLLY 243

RESULT 13
US-08-463-911-4
; Sequence 4, Application US/08463911
; Patent No. 5869330
; GENERAL INFORMATION:
; APPLICANT: Scherer, Philipp E.
; APPLICANT: Lodish, Harvey E.

; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463.911
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI95-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-463-911-4

Query Match 20.08; Score 274; DB 2; Length 246;
Best Local Similarity 31.38; Pred. No. 7.6e-20;
Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;

QY 51 GYQPPGPPGPGIPGNHNGNNGATGHH-----EGAKGKGDGLGPRGERGHPK 104
Db 32 GYQPPGPPGPGIPGNHNGNNGATGHH-----EGAKGKGDGLGPRGERGHPK 91
QY 105 GEKGYPIP-----PELQ-----IAFMASLATHFSNQSGIIFSSVETNIGNF 147
Db 92 GTSGLPGDPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG 151
QY 148 FDMVTGRGAPVSGVYFFTFESMMKHEDVEEVYVLMHNGNTVFSM-----YSYEMK 198
Db 152 YNPSTGKFTCEVGLYFYV-----YTSHANLCVHLNLNARVASFCDHMF 198
QY 199 GKSDTSSNHAHLKAKGDEVWLRM--NGALHGDHOREFSTAGFLFLF 243
Db 199 NSKQVSSGALLRLQRGDEVWLSVNDYNGMV-GIEGNSVFSGLFLF 244

RESULT 14
US-09-370-838-185
; Sequence 185, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370.838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289

Search completed: January 13, 2003, 10:44:35
Job time : 17 secs

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-185

Query Match 20.0%; Score 273; DB 4; Length 746;
Best Local Similarity 29.6%; Pred. NO. 4.4e-19;
Matches 72; Conservative 43; Mismatches 90; Indels 38; Gaps 8;

QY	34	GLPPDCSKCHGDYS-----FRGYQGP-----GPPGPGIPGNGHNGNN	74
DB	509	GLP-----SISNGYSQLQFAREYSGAPYSQRDNFQOCYKRGTSGGPRANSRAGWSDS	564
QY	75	GATGHEGAKGKGDGLGPRGERGQ-----HGPKGE-----KGYPGIPPELQIAFMAS	123
DB	565	QVSSPE-RNETFNSGDSGQDSRSMTDVDVPTNPAATILPVHYVP-LPQOMRVAFSAA	622
QY	124	LATHFS--NONSGIIFSSVETNIGNFDMTGRGAPVSGVYFFTFSSMMKHEDVEEYVY	181
DB	623	RTSNLAPGTLDPQIIVFDLLNNLIGETFDLQGRFNCVNGTYVFIHMLKLAVNVPVLYN	682
QY	182	LMHNGNTVFSMYEMKSKSDTSSNHAVLKAGDEWLMRMNGALHGDHQRFTFAGEL	241
DB	683	LMRNEVLVSAYANDGAPDHETASNAIQLFQGDQIWLRLHGAIGSSWKYSTFSGYL	742
QY	242	LFE 244	
DB	743	LYQ 745	

RESULT 15
US-09-336-536-4
; Sequence 4, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-4

Query Match 19.3%; Score 264.5; DB 4; Length 228;
Best Local Similarity 32.4%; Pred. No. 6.3e-19;
Matches 68; Conservative 36; Mismatches 79; Indels 27; Gaps 7;

QY	56	PGPPGPGIPGNGHN-----NGNGATGHEGAKGKGD-----KGDGPRGERGQ	100
DB	14	PGHPLGPTGHHGVSQGLPGRDGRDRCAPGAPGKGGGRGPGPGPRGEAGP	73
QY	101	HGPKEGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFDMTGRFAPVS	160
DB	74	AGPTGPGCECVPPRSAPSAKRSRSPVPPSDAPLPFDRLVNEQGHGDAVTGKFTCOVP	133
QY	161	GVYFTFSMMKHEDVEEYVY--LMHNGNTVFSMYEMKG--KSDTSSNHAVLKLAGD	216
DB	134	GVYFAV-----HATVYRASLQFDLVKNGESTASFQF-FGWPAPASLSCGAMVRLPED	188
QY	217	EWLRLMNG---ALHGDHQRFTFAGFLLF	243
DB	189	QWVQVGVGDYIGIYASIKTDTSTSGFLVY	218

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:42:03 ; Search time 19 Seconds
(without alignments)
1244.688 Million cell updates/sec

Title: US-09-931-836-2
Perfect score: 1367
Sequence: 1 LMWRQLIYWQLLALFFLPFC.....LHGDRQRFSTFAGFLLETK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293.5	21.5	244	JC4708	gelatin-binding 28
2	280.5	20.5	674	S3297	collagen alpha 1(X
3	278.5	20.4	680	S31216	collagen alpha 1(X
4	275	20.1	674	S13301	collagen alpha 1(X
5	274	20.0	246	S29328	complement subcomp
6	270	19.8	680	CGHU1D	collagen alpha 1(X
7	264.5	19.3	219	T14782	hypothetical prote
8	258.5	18.9	744	A34246	collagen alpha 1(V
9	255.5	18.8	744	S15435	collagen alpha 1(V
10	255	18.7	245	C1HUQC	complement subcomp
11	251.5	18.4	253	C1HUQB	complement subcomp
12	251.5	18.4	744	S23298	collagen alpha 1(V
13	249	18.2	635	A57131	collagen alpha 2(V
14	248	18.1	743	S23779	collagen alpha 1(V
15	239.5	17.5	245	S39018	complement subcomp
16	236.5	17.3	253	S49158	complement protein
17	231.5	16.9	253	S49560	complement Clq B c
18	226	16.5	423	A55797	collagen precursor
19	219	16.0	245	C1HUQA	complement subcomp
20	216	15.8	920	A45748	collagen alpha 1(V
21	215	15.7	992	T08772	hypothetical prote
22	211.5	15.5	366	S11449	collagen short cha
23	210.5	15.4	423	A41207	collagen 13, nonfi
24	208	15.2	2944	A54849	collagen alpha 1(V
25	207.5	15.2	775	A61228	collagen alpha 2(I
26	207.5	15.2	1549	T48103	type VII collagen
27	203.5	14.9	1707	A33526	collagen alpha 2(I
28	203.5	14.9	1712	CGHU2B	collagen alpha 2(I
29	202	14.8	215	B48150	hibernation-relate

hibernation-relate
collagen alpha 1(I
cerabellin-like gl
collagen alpha 1(X
collagen alpha 1(X
collagen alpha 1(I
collagen 1 - Caeno
hypothetical prote
collagen alpha 1(I
collagen alpha 1(I
hypothetical prote
cerabellin precurs
pulmonary surfacta
collagen alpha 1(I
collagen alpha 1(I
collagen alpha 1(X

ALIGNMENTS

RESULT 1

JC4708

gelatin-binding 28K protein precursor - human

N:Alternate names: adipose specific collagen-like factor

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999

C:Accession: JC4708; JC4944

R:Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.

Biochem. Biophys. Res. Commun. 221, 286-289, 1996

A:Title: cDNA cloning and expression of a novel adipose specific collagen-like factor

A:Reference number: JC4708; MUID:96224171; PMID:8619847

A:Accession: JC4708

A:Molecule type: mRNA

A:Residues: 1-244 <NA>

A:Cross-references: DBJ:D45371; NID:g871886; PID:BAA08227.1; PID:g871887

A:Experimental source: adipose tissue

R:Nakano, Y.; Tobe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M.

J. Biochem. 120, 803-812, 1996

A:Title: Isolation and characterization of GBP28, a novel gelatin-binding protein pur

A:Reference number: JC4944; MUID:97103474; PMID:8947845

A:Accession: JC4944

A:Molecule type: protein

A:Residues: 19-38;93-100;101-112;135-149;173-178 <NA>

C:Comment: This protein is an endogenous factor that binds with a collagen-like domain

C:Genetics:

A:Gene: apM1

C:Superfamily: unassigned collagens; complement Clq carboxyl-terminal homology

C:Keywords: adipose tissue; glycoprotein; hydroxyproline

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-244/Product: gelatin-binding 28kDa protein #status experimental <MAT>

F:42-107/Region: collagen-like

F:114-241/Domain: complement Clq carboxyl-terminal homology <CIQ>

F:95/Modified site: 4-hydroxyproline (Pro) #status experimental

F:230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 21.5%; Score 293.5; DB 2; Length 244;

Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PCPPCP-----PGIPGNHGNNGNNGATGHEGAKGKDGKD---LGPR---GE 97

Db 23 QGPGVLLPLPKGACTGWNAGIPGPHNGAGPGRDGTTPGKGEKGDPLGIGKDGIGE 82

QY 98 RQHGPKGKGYPGT-----PPE-----LQIAFMASLATHFSNQNSGIFFSVETNIGNF 147

Db 83 TGVPCAEGPRGPGGLOGRKGEGEGAYVRSFVGLTYVTIPNMPRTFTIFFVNOQH 142

QY 148 FDMVTGRGAPVSGVYFFTFSSMKHEDVEVYVYLMHNGNTVFSMYSEMKGKSDTSSNH 207

Db 143 YDGSYGKFCNIPGLYFYFAYHITVY--MKDKVSLFKKDKAMLFYDQVQENNVDQASGS 200

QY 208 AVLKLAKGDEWLRM--GNG---ALHGDHQRFTSTFAGFLLF 243

Db 503 EPLGPPGPPGPPGQAVMPDGFKAGQRPRLSGMPLVSANHGVTGMPVSAFTVILSKAY 562
Qy 129 SNQSGIIFSSVETNIGNFDDVMTGRFGAPVSGVYFFTFSSMMKHEDVEEVYVLMHNGNT 188
Db 563 PAVGAPIFDELYNRQOHYDPRSGIFTCKPIGIYFYSYHV--HVKGTHVMVGLYKNGTTP 620
Qy 189 VFSWYSYE--MKGSDTSSNIAVLKLAGDEWVLRMGN---GALHGDHQRSTFAGFL 242
Db 621 --TWTYDEYSKGYLDQASGAIMELTENDQVWLQLPNAESNGLYSSSEYVHSSFSGLFV 677

RESULT 4

S13301
collagen alpha 1(X) chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
C:Accession: S13301
R:Thomas, J. T.; Kwan, A. P. L.; Grant, M. E.; Boot-Handford, R. P.
Biochem. J. 273, 141-148, 1991
A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. EV
A:Reference number: S13301; MUID:91113131; PMID:1703407
A:Accession: S13301
A:Molecule type: mRNA
A:Residues: 1-674 <THO>
A:Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
C:Genetics:

A:Gene: COL10A1
C:Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
C:Keywords: coiled coll; extracellular matrix; glycoprotein; homotrimer
F:1-18/Domain: signal sequence status predicted <SIG>
F:19-674/Product: collagen alpha 1(X) chain status predicted <MAT>
F:547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>

Query Match 20.1%; Score 275; DB 2; Length 674;
Best Local Similarity 30.0%; Pred. No. 6.6e-15;
Matches 72; Conservative 31; Mismatches 87; Indels 50; Gaps 6;

Qy 51 GYQGPDPGPPGPGIPGPNHNGNNGATGHEGAKGEKD-----KGDLPGRGERG 99
Db 434 GHNGEAGRGVPGIPGTRGPIGPPGPGSGKGDVGTGPPGPAIAVKGNGLTGPPG 493
Qy 100 QHCPKEKGYGPIP-----PELQIA----FMASLATHFSNONSGII----- 136
Db 494 PPGPRNAGEPLGPPGPPGPGQVALPEDFVKAGQRFVSNQGVGTGMPVSAFTVILS 553
Qy 137 -----FSSVETNIGNFDDVMTGRFGAPVSGVYFFTFSSMMKHEDVEEVYVLMHN 185
Db 554 KAYPAIGTPIPFKILYNKQHYDPRGTGIFTCKPIGIYFYSYHI--HVRGTHAWVGLYKN 611
Qy 186 GNTVFSMYSYEMKGSDDTSSNHAVALKLAGDEVWLRM---GNCALHGDHQRSTFAGFL 242
Db 612 GTPVMYTYDEYIKGYLDQASGSAVIDLTENDQVWLQLPNAGSNGLYSPEYVHSSFSGLFV 671

RESULT 5

S29328
complement subcomponent Clq chain C - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S29328
R:Petty, F.; Reid, K. B. M.; Loos, M.
Eur. J. Biochem. 209, 129-134, 1992
A:Title: Isolation, sequence analysis and characterization of cDNA clones coding for the
earebellin.
A:Reference number: S29328; MUID:93011118; PMID:1396691
A:Accession: S29328
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-246 <PET>

A:Cross-references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229
C:Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hom
F:122-245/Domain: complement Clq carboxyl-terminal homology <ClQ>

Query Match 20.0%; Score 274; DB 2; Length 246;
Best Local Similarity 31.3%; Pred. No. 2.8e-15;
Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;
Qy 51 GYQGPDPGPPGPGIPGPNHNGNNGATGH-----EGAKGEKGDGLGPRGERGQHGP 104
Db 32 GCYGIPIGPNPGAPGKGDHGLQPKGPGEPGIPAVPGTQGPQKGGKGEPMGHRGKNGPR 91
Qy 105 GEKYPGPIP-----PELQ-----TAFMASLATHFSNONSGIIFSSVETNIGNF 147
Db 92 GTSGLPGDPGRPGPEGVEGRYKQKHQSVFTTROTQYPEANALVRFSNVVTNPOGH 151
Qy 148 FDMVTGRFGAPVSGVYFFTFSSMMKHEDVEEVYVLMHNGNTVFSM-----YSYEMK 198
Db 152 YNPSTGKTCFVPGIYFYV-----YTSHATANCLVHLNLNLARVASEFCDHMF 198
Qy 199 GKSDTSSNHAVALKLAGDEVWLRMG--NGALHGDHQRSTFAGFLF 243
Db 199 NSKQVSSGGALLRLQRGDEVWLSVNDYNGMV-GIEGSNSVFGFLF 244

RESULT 6

CCHUID
collagen alpha 1(X) chain precursor - human
N:Alternate names: procollagen alpha 1(X) chain
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
C:Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R:Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B. R.; von der Mark, K.; Bertling,
FBBS Lett. 311, 305-310, 1992
A:Title: Genomic organization and full-length cDNA sequence of human collagen X.
A:Reference number: S26396; MUID:93012005; PMID:1397333
A:Accession: S26396
A:Molecule type: DNA
A:Residues: 1-680 <REI>
A:Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714; GB
R:Apte, S.S.
submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30086
A:Molecule type: DNA
A:Residues: 'TTPFYGVWCWVCL', 52-680 <APT>
A:Cross-references: EMBL:X65120; NID:g23129
A:Note: the initial difference is probably due to translation of an intronic sequence
R:Apte, S.; Mattel, M.G.; Olsen, B.R.
FBBS Lett. 282, 393-396, 1991
A:Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gen
A:Reference number: S15826; MUID:91243838; PMID:2037056
A:Accession: S15826

A:Molecule type: DNA
A:Residues: 561-647, 'G', 649-666 <AP2>
A:Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA1686.1; PID:g30014
R:Thomas, J. T.; Cresswell, C. J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant
Biochem. J. 280, 617-623, 1991
A:Title: The human collagen X gene. Complete primary translated sequence and chromoso
A:Reference number: S18249; MUID:92109659; PMID:1764025
A:Accession: S18249

A:Molecule type: DNA
A:Residues: 1-26, 'T', 28-680 <THO>
A:Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-
R:Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
Dev. Biol. 148, 562-572, 1991
A:Title: In situ hybridization studies on the expression of type X collagen in fetal
A:Reference number: A43901; MUID:92077285; PMID:1743401
A:Accession: A43901
A:Molecule type: mRNA
A:Residues: 547-656 <RE2>
A:Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A:Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBI:P:69014)
R:Wallis, G. A.; Rash, B.; Sweetman, W. A.; Thomas, J. T.; Super, M.; Evans, G.; Grant,
Am. J. Hum. Genet. 54, 169-178, 1994
A:Title: Amino acid substitutions of conserved residues in the carboxyl-terminal doma

A:Residues: 28-99, P', 101-195 <RE3>
R:Reid, K.B.M.; Gagnon, J.; Frampton, J.
Biochem. J. 203, 559-569, 1982
A:Title: Completion of the amino acid sequences of the A and B chains of subcomponent Cl
A:Reference number: A90315; MUID:82283890; PMID:6981411
A:Accession: B90315
A:Molecule type: protein
A:Residues: 136-253 <RE4>
A:Note: 176-Glx may also be present
C:Comment: The first component of complement is a calcium-dependent complex of the three
activation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement.
C:Comment: The C1q subcomponent is composed of nine subunits, six of which are disulfide
(see PIR.C1HUQC) chain. Equimolar amounts of the A, B, and C chains are found after red
A:Gene: GDB:C1QB
A:Cross-references: GDB:119043; OMIM:120570
A:Map position: lp36.3-lp34.1
C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom
F:1-27/Domain: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-253/Product: complement subcomponent C1q chain B #status experimental <MAT>
F:123-116/Domain: collagenous, triple helix <COL>
F:123-249/Domain: complement C1q carboxyl-terminal homology <C1Q>
F:28/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F:31/Disulfide bonds: interchain (to chain A-26) #status experimental
F:35,38,41,53,56,85,93,86,101,104,107/Modified site: 4-hydroxyproline (Pro) #status exp
F:59,62,77,92,98,110/Modified site: 5-hydroxylysine (Lys) #status experimental
F:59,62,98,110/Binding site: carbohydrate (Lys) (covalent) #status experimental
Query Match 18.4%; Score 251.5; DB 1; Length 253;
Best Local Similarity 31.7%; Pred. No. 2.1e-13;
Matches 73; Conservative 27; Mismatches 89; Indels 41; Gaps 6;
QY 43 CHGYSFRGYQGPDPGP-----PGIPGNHNGNNGATGHEGAKGKGDGLGRGERG 99
Db 31 CTGPPAIPGIPGTPGDPGPQGPPIGKGLPLGLAGDHGEGKGDGPIGNPKVG 90
QY 100 QHGPKEGYGPDP-----PELQIAFWASLATHFS-NQNSGIIFSSVETNIG 145
Db 91 PKGPMGKGGGAGCAGCPKESGDYKATOKIAFSARTINVPRLRDOTIRFDHVIITNM 150
QY 146 NFFDVTGFRGAPYSGVYFFTFSS-----MKHEDVEEYVYLMHNGNTVFSMYS 194
Db 151 NNYEPRSGKFTCKVPLGYLYFTYHASSRGNLCVNLMRGERAKQVVTCDYAYNFF----- 205
QY 195 YEMKGSDDTSSNHAVALKAGDEWLR-MGNALHGDHQRFTFAGFLF 243
Db 206 -----QVTTGGMVLKLEQENVFLOATDKNSLLMEGANSIFSGLLF 248
RESULT 12
S23298
collagen alpha 1(VIII) chain - chicken
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Accession: S23298
R:Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; Mc
machugi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre
A:Title: The molecular biology of collagens with short triple-helical domains.
A:Reference number: S22243
A:Accession: S23298
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-744 <NIN>
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>
Query Match 18.4%; Score 251.5; DB 1; Length 744;
Best Local Similarity 29.9%; Pred. No. 6.2e-13;
Matches 78; Conservative 24; Mismatches 104; Indels 55; Gaps 6;
QY 34 GLPPDCKCHGDYSGRQYQGPDPGPPIGNHNGNNGATGHEGA-----KCE 85

Db 486 GIPGD--OGLQPPGIPGTPSGIPGIPGPGKGGPLGPPGPGVGRPGVAGLHGP 543
QY 86 KGDGDLGRGERGQHGKPKGKGYPGIP-----PELQI----- 118
Db 544 PGKPGALGPQGPGLGPPGPPGPPGPPVMPPTAPQGEYLPDMGLGIDGKVTPHAYAA 603
QY 119 -----AFMASLATHFSNQNSGIIFSSVETNIGNFFDVTGFRGAPYSGVYFF 165
Db 604 KKGNGGPAYEMPATFALTAPFPVGPAPIKFDRLLYNGRONYNPTGIFTCEVPGVYF 663
QY 166 TFSMMKHEDVEEYVYLMHNGNTVFSMYSEYMKKSDTSSNHAVALKAGDEWLRMGN- 224
Db 664 AYHV-HCKGNNVVALFKNNEPVWYFYDEYKKGFLQOASGSAVLLLRPGDRVFLQNPSE 721
QY 225 --GALHGDHQRFTFAGFLF 243
Db 722 QAAGLYAGQYVHSSFSGYLLY 742
RESULT 13
A57131
collagen alpha 2(VIII) chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
C:Accession: A57131
R:Muraqaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.
J. Biol. Chem. 266, 7721-7727, 1991
A:Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen f
A:Reference number: A57131; MUID:91210292; PMID:2019595
A:Accession: A57131
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-635 <MUR>
A:Cross-references: GB:M60832; NID:g17178; PIDN:AAA62822.1; PID:g17179
C:Genetics:
A:Gene: GDB:COL8A2
A:Cross-references: GDB:127812; OMIM:120252
A:Map position: lp34.3-lp32.3
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:1-11/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>
F:12-468/Region: interrupted helical
F:469-635/Domain: carboxyl-terminal nonhelical #status predicted <NC7>
F:508-634/Domain: complement C1q carboxyl-terminal homology <C1Q>
Query Match 18.2%; Score 249; DB 2; Length 635;
Best Local Similarity 30.8%; Pred. No. 8.5e-13;
Matches 76; Conservative 25; Mismatches 94; Indels 52; Gaps 7;
QY 45 GDYSFRGYQGPDPGPPIGNHNGNNGATGHEGAKGKGDGLGRGERGQHPK 104
Db 395 GPSGIPGLQGPAGPIGPQGLGKLPGLGPPG-ESRAGEPTAGPRGPPGSPG 453
QY 105 GEKGYGPDP-----PELQI-----AFMASL 124
Db 454 GPPGLGPPGAPCAFDETGTAGLHLPNGVGEAVLGKGGKPPQGLGELSAHAHTPAFTAVL 513
QY 125 ATHFSNQNSGIIFSSVETNIGNFFDVTGFRGAPYSGVYFFTFSSMMKHEDVEEYVYLMH 184
Db 514 TSPLPASGMPVFDRTLYNGHSGYNPATGIFTCPGVGVYFAY-----HVHVKGTVNWWAL 569
QY 185 NGNTVFSMYSE--MKGKSDTSSNHAVALKAGDEWLRM-----GNGALHGDHQRFTSFA 238
Db 570 YKNNVPATYTYDEYKKGVLQOASGGAVALQRLRPDQVWQIPSDQANG-LYSTEYIHSSFS 628
QY 239 GFLLFET 245
Db 629 GFLLCPT 635
RESULT 14
S23779
collagen alpha 1(VIII) chain - mouse

```

Qy 212 LKRGDEVWLRM--GNCALHGDHORFSEFAGLELF 243
      |.:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 209 LRRGDEVWIEKDFAKGRIOYGTADSIFSGLIF 242

```

search completed: January 13, 2003, 10:44:13
Job time : 20 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:31:58 ; Search time 12 Seconds

(without alignments)

850.265 Million cell updates/sec

Title: US-09-931-836-2

Perfect score: 1367

Sequence: 1 MLNRQLIYWQLLALFLPFC.....LHGDHQRFTFAGLLPFTK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1367	100.0	246	1 CQT3_HUMAN	Q9bxj4 homo sapien
2	315	23.0	289	1 COT7_HUMAN	Q9bx12 homo sapien
3	304	22.2	285	1 COT2_HUMAN	Q9bx15 homo sapien
4	297.5	21.8	258	1 C1RF_HUMAN	O75973 homo sapien
5	297.5	21.8	258	1 C1RF_MOUSE	O88992 mus musculus
6	294	21.5	247	1 APM1_MOUSE	Q60994 mus musculus
7	293.5	21.5	244	1 APM1_HUMAN	Q15848 homo sapien
8	289.5	21.2	278	1 COT6_HUMAN	Q9bx19 homo sapien
9	285.5	20.9	255	1 GLIC_MOUSE	O9esn4 mus musculus
10	280.5	20.5	674	1 CALA_CHICK	P08125 gallus gall
11	278.5	20.4	680	1 CALA_MOUSE	Q05306 mus musculus
12	275	20.1	674	1 CALA_BOVIN	P23206 bos taurus
13	274	20.0	246	1 C1QC_MOUSE	Q02105 mus musculus
14	270	19.8	680	1 CALA_HUMAN	Q03692 homo sapien
15	264.5	19.3	243	1 COT5_HUMAN	Q9bx10 homo sapien
16	258.5	18.9	744	1 CAL8_RABIT	P14282 oryctolagus
17	257.5	18.8	744	1 CAL8_HUMAN	P27658 homo sapien
18	257	18.8	743	1 CAL8_MOUSE	Q00780 mus musculus
19	255	18.7	245	1 C1QB_MOUSE	P02747 homo sapien
20	254	18.6	419	1 COLE_LEPMA	P98085 lepomis mac
21	251.5	18.4	251	1 C1QB_HUMAN	P02745 homo sapien
22	249	18.2	635	1 CA28_HUMAN	P25067 homo sapien
23	239.5	17.5	245	1 C1QA_MOUSE	P98086 mus musculus
24	236.5	17.3	253	1 C1QB_RAT	P31721 rattus norv
25	231.5	16.9	253	1 C1QB_MOUSE	P14106 mus musculus
26	226	16.5	281	1 COT1_HUMAN	Q9bxj1 homo sapien
27	219	16.0	245	1 C1QA_HUMAN	P02745 homo sapien
28	211.5	15.5	366	1 CAS4_EPHMU	P16503 ephydratia m
29	208	15.2	2944	1 CAL7_HUMAN	Q02388 homo sapien
30	203.5	14.9	1707	1 CA24_MOUSE	P08122 mus musculus
31	203.5	14.9	1712	1 CA24_HUMAN	P08572 homo sapien
32	202	14.8	215	1 HP25_TAMSI	Q06576 tamias sibi
33	201	14.7	215	1 HP27_TAMSI	Q06577 tamias sibi

34	200	14.6	1516	1 CALH_HUMAN	P39060 homo sapien
35	196	14.3	224	1 CERL_RAT	P98087 rattus norv
36	195.5	14.3	1527	1 CALH_MOUSE	P39061 mus musculus
37	195	14.3	458	1 COLQ_RAT	O35167 rattus norv
38	193.5	14.2	1758	1 CAL4_CAEL	P17139 caenorhabdi
39	193	14.1	296	1 CC01_CAEL	P08124 caenorhabdi
40	193	14.1	456	1 COLQ_HUMAN	Q9y215 homo sapien
41	192	14.0	1466	1 CAL3_HUMAN	P03461 homo sapien
42	189	13.8	193	1 CERB_HUMAN	P23435 homo sapien
43	189	13.8	193	1 CERB_MOUSE	Q9r171 mus musculus
44	189	13.8	375	1 PSPD_HUMAN	P35247 homo sapien
45	189	13.8	1464	1 CAL3_MOUSE	P08121 mus musculus

ALIGNMENTS

RESULT 1

CQT3_HUMAN

ID CQT3_HUMAN STANDARD; PRT; 246 AA.

AC Q9BXJ4; Q96KY1;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Complement-clq tumor necrosis factor-related protein 3 precursor

DE (Secretory protein COR526).

GN C1QTNF3 OR CTRP3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Piddington C.S., Bishop P.;

RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RA Maeda T., Hayashi A., Saito T.;

RT "Molecular cloning, chromosomal localization, and genomic structure of

the human COR526 gene.";

[3]

RP Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RC SEQUENCE OF 121-246 FROM N.A.

TI SSUE=Placenta;

RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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CC EMBL; AF329837; AAK17961.1; -

DR EMBL; AF326976; AAK70344.1; -

DR EMBL; BC016021; AAH16021.1; -

DR EMBL; HGNC:14326; C1QTNF3.

DR InterPro; IPR001073; C1q.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF00386; C1q; 1.

DR Pfam; PF01391; Collagen; 1.

```
FT DOMAIN 51 113 COLLAGEN-LIKE.
FT DOMAIN 114 246 C1Q.
FT CONFLICT 214 214 K -> E (IN REF. 3).
SQ SEQUENCE 246 AA; 26994 MW; C589B6C3A73E5D29 CRC64;

Query Match 100.0%; Score 1367; DB 1; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNRQLYVWLLALFFLPCLCODEYVESQTLGGLPPDCSKCHGDSYFRGYGPPGPPG 60
   |||||||
Db 1 MLNRQLYVWLLALFFLPCLCODEYVESQTLGGLPPDCSKCHGDSYFRGYGPPGPPG 60
   |||||||

QY 61 PPGIPGNHGNNGGATGHEGAKGERGDKGLGPRGERGQHGPKGYPGIPPELQIAF 120
   |||||||
Db 61 PPGIPGNHGNNGGATGHEGAKGERGDKGLGPRGERGQHGPKGYPGIPPELQIAF 120
   |||||||

QY 121 MASLATHFSNQNGIIFSSVETNIGNFDMVMTGRFGAPVSGVYFTFSMMKHEDVEVYV 180
   |||||||
Db 121 MASLATHFSNQNGIIFSSVETNIGNFDMVMTGRFGAPVSGVYFTFSMMKHEDVEVYV 180
   |||||||

QY 181 YLMHNGNTVFSMYEMKGSDFSSSHAVLKLAKGDEVWLMRGMGALHGDHQRFFSTFAGF 240
   |||||||
Db 181 YLMHNGNTVFSMYEMKGSDFSSSHAVLKLAKGDEVWLMRGMGALHGDHQRFFSTFAGF 240
   |||||||

QY 241 LLEFETK 246
   |||||||
Db 241 LLEFETK 246
   |||||||

RESULT 2
CQT7_HUMAN STANDARD; PRT; 289 AA.
ID CQT7_HUMAN
AC Q9BXJ2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Complement-clq tumor necrosis factor-related protein 7 precursor.
GN C1QTNF7 OR CTRP7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.;
RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF329839; AAK17963.1; -
CC EMBL; BC022187; AAH22187.1; -
CC Genew; HGNC:14342; C1QTNF7.
CC InterPro; IPR001073; Clq.
CC Pfam; PF00386; Clq; 1.
CC Pfam; PF01391; Collagen; 2.
CC PRINTS; PR00007; COMPLENNTC1Q.
CC SMART; SM00110; Clq; 1.
```

```
DR PROSITE; PS01113; C1Q; 1.
KW Collagen; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 289 COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
   RELATED PROTEIN 7.
FT DOMAIN 38 139 COLLAGEN-LIKE.
FT DOMAIN 141 276 C1Q.
SQ SEQUENCE 289 AA; 30683 MW; A61609FF86D26946 CRC64;

Query Match 23.0%; Score 315; DB 1; Length 289;
Best Local Similarity 30.1%; Pred. No. 1.3e-19;
Matches 86; Conservative 32; Mismatches 96; Indels 72; Gaps 9;

QY 14 LFLFLPCLCODEYVESQTLGGLPPDCSKCHGDSYFRGYGPPGPPGIPGNHGNNGN 73
   |||:|:|
Db 5 LYVTSFAICASGQPRGNQLKGENYSPRYIC----SIPGLPGPPGPGANGSPGPHGRIGL 60
   |||:|:|

QY 74 NGATGHEGAKGERGDKGLGPRGERGQHGPKGYPGIPPELQIAF 103
   |||:|:|
Db 61 PGRDGRGRGKGEKGTAGLGRKGTGLGAGEKGDQGETGKKGPIGPEGEKGEVGP 120
   |||:|:|

QY 104 -----KGEKGYGIPP-----ELQIAFMASLATHFSNQNGIIFSSVETNIGNFEDV 150
   |||:|:|
Db 121 PGKGRGRGEGDGLPGVCRGSGIVLKSAFSGVITTSPEERLPITFNKVLFEHGHYNP 180
   |||:|:|

QY 151 MTGRFGAPVSGVYFTFSMM---KHEDVEEVYVYLMHNGNTVFSMYSEYEMK-----GKS 201
   |||:|:|
Db 181 ATGKFICAPGIYFSDITLANKH-----LAIGLVHNG-----QYRIKTFDANTGNH 228
   |||:|:|

QY 202 DTSSNHAVLKLAKGDEVWLMR-----NGALHGDHQRFFSTFAGFLF 243
   |||:|:|
Db 229 DVASGSTVIYLOPEDEVWLEIFFTDQNLGFLSDPGWADSLFSGFLY 274
   |||:|:|

RESULT 3
CQT2_HUMAN STANDARD; PRT; 285 AA.
ID CQT2_HUMAN
AC Q9BXJ5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Complement-clq tumor necrosis factor-related protein 2 precursor.
GN C1QTNF2 OR CTRP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Piddington C.S., Bishop P.;
RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RA TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF329836; AAK17960.1; -
CC EMBL; BC011699; AAH11699.1; -
CC Genew; HGNC:14325; C1QTNF2.
CC InterPro; IPR001073; Clq.
CC InterPro; IPR000087; Collagen.
```

```
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 2.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; Clq; 1.
DR PROSITE: PS01113; Clq; 1.
KW Collagen; Signal.
FT SIGNAL 1 15
FT CHAIN 16 285
FT DOMAIN 40 141
FT DOMAIN 143 285
SQ SEQUENCE 285 AA; 2952 MW; 7E31FF9868D4EDFA CRC64;

Query Match 22.2%; Score 304; DB 1; Length 285;
Best Local Similarity 29.6%; Pred. No. 1.1e-18;
Matches 73; Conservative 42; Mismatches 74; Indels 58; Gaps 9;

QY 48 SFRGQGGPPGPPGPP-----GIP---GNHNGNNGNATGHEGAKGKGDGLQPR 95
DB 37 SLPGQGGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP 96
QY 96 GER-----GQHGPKGKGYGIP-----PELQIAFMASL 124
DB 97 GKAGAGRAGPRKGVNGTGGKHTGKGGKPKGKGGKGGKGGKGGKGGKGGKGGKGG 156
QY 125 ATHFSNQSGIIFSVETNIGNFFDMTGRFGAPVSGVYFFTFMM---KHEDVEEVYV 181
DB 157 TKSYPRLRPIKFDKILNNEGHYNASSGKFCVGVGYIYFYDITLANKH-----LAIG 211
QY 182 LMHNGNTVFSMYSEMK-GKSDTSNHAFLKAKGDEVLRLM-----GNGLHGDHQRFT 236
DB 212 LVHNGQ---YRITFDANTGNHDVASGSTITALKQGEVWLQIFYSEQNGLFYDPYWTDSL 269
QY 237 FAGLLF 243
DB 270 FTGFLIY 276

RESULT 4
CIRF_MOUSE
ID CIRF_MOUSE STANDARD; PRT; 258 AA.
AC O75973;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Clq-related factor precursor.
GN ClQRF OR CRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99097006; PubMed=9878755;
RA Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko V.,
RA Baskin D.S., Smith J.R., Pereira-Smith O.M.;
RA "Cloning and characterization of CRF, a novel Clq-related factor,
RT expressed in areas of the brain involved in motor function.";
RL Brain Res. Mol. Brain Res. 63:233-240(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT IN AREAS
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 ClQ DOMAIN.
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: AF095154; AAC64186.1; -
DR EMBL: AF410771; AAK95248.1; -
DR EMBL: BC008798; AAR08798.1; -
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 1.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; Clq; 1.
DR PROSITE: PS01113; Clq; 1.
KW Collagen; Signal.
FT SIGNAL 1 16
FT CHAIN 17 258
FT DOMAIN 67 115
FT DOMAIN 123 258
FT DOMAIN 123 258
SQ SEQUENCE 258 AA; 26452 MW; 52C51CDF59CAE2BF CRC64;

Query Match 21.8%; Score 297.5; DB 1; Length 258;
Best Local Similarity 34.2%; Pred. No. 3.5e-18;
Matches 76; Conservative 32; Mismatches 89; Indels 25; Gaps 8;

QY 29 SPQTGLPDCSKCHGDYSFRGYQPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP 88
DB 53 SPQSGAPP--STLVQGGQGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 101
QY 89 KGDLPGRG--ERQHGPKGKGYGPIPPQLQIAFMASLATHFSNONG---IFSSVETN 143
DB 102 PGKPGPPGLPGAGSGAISTATYITVP---RVAFYAGL---KNPREGYEVLFKDFDDVVTN 154
QY 144 IGNEFDVMTGRFGAPVSGVYFFTFES-MKKHEDVEEVYVLMHNGNTVFSMYSEMKGKSD 202
DB 155 LGNNYDAASGRFTCNIPGTIFYHVMRGDGTSMWADLCNKGQVRSAAIAQADQNDY 214
QY 203 TSSNHAFLKAKGDEVLRLMNGALH-GDHQRFSTFAGFLF 243
DB 215 YASNSVILHLDAGDEVFIKLDGGKAHGNSKNYSFSGFIY 256

RESULT 5
CIRF_MOUSE
ID CIRF_MOUSE STANDARD; PRT; 258 AA.
AC O88992;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Clq-related factor precursor.
GN ClQRF OR CRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99097006; PubMed=9878755;
RA Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko V.,
RA Baskin D.S., Smith J.R., Pereira-Smith O.M.;
RA "Cloning and characterization of CRF, a novel Clq-related factor,
RT expressed in areas of the brain involved in motor function.";
RL Brain Res. Mol. Brain Res. 63:233-240(1999).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT IN AREAS
CC OF THE NERVOUS SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS THE
CC PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUCLEUS,
CC THE PONS AND THE RED NUCLEUS.
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 ClQ DOMAIN.
-----
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CC -----
DR EMBL: U37222; AAA80543.1; -
DR EMBL: U49915; AAB06706.1; -
DR EMBL: AF304466; AAK13417.1; -
DR EMBL: AK003138; BAB22597.1; -
DR MGD: MGI:106675; ACRP30.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 1.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR Hormone; PS01113; C1Q; 1.
KW Polymorphism. 1 17
FT SIGNAL 18 247
FT CHAIN 18 247
FT DOMAIN 45 110
FT DOMAIN 111 247
FT DISULFID 39 39
FT MOD_RES 47 47
FT MOD_RES 50 50
FT MOD_RES 56 56
FT MOD_RES 65 65
FT MOD_RES 79 79
FT MOD_RES 98 98
FT MOD_RES 107 107
FT VARIANT 113 113
FT CONFLICT 50 50
FT CONFLICT 74 74
FT CONFLICT 117 117
FT CONFLICT 148 148
FT CONFLICT 243 243
SO SEQUENCE 247 AA; 26841 MW; 137B687D873988C4 CRC64;

Query Match 21.5%; Score 294; DB 1; Length 247;
Best Local Similarity 31.5%; Pred. No. 6.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

Qy 6 LIYWOLLALFPLFCODEYMESPQTGG--LPPDCSKCHGYSFRGYGPPGPPGPPG 63
Dy 2 LLLQALLPLLIP-SHAEDVTTTEELAPALVPPPKGTCA-----CWMA-----GIPG 48
Qy 64 IPGNHNGNNGATGCEKGEKGDGLGRGER---GQHGPKGEKYPGIPPR----- 115
Dy 49 IPGHNGTPGRDGRDGTGPKGEKGDAGLLGPKGETGDVGMTCAGPRGPGTGRKGRPG 108
Qy 116 -----LQIAFNASLATPNSQNSGIFFSVETNIGNFDDVMTGFRGAPVSGVYFFTESMM 170
Dy 109 EAAVYRSFASVGLTRVTVNVPFRFKIFYNQONHYDGTGKPYCNPGLYFYSYHIT 168
Qy 171 KHEDEVEVYVLMHNGNTVFSMYEMKGSQDTSNHAVLKLAGDEYWLRM-GNG---A 226
Dy 169 VY--MKDVKVSLEFKDKAVLFTYDQYQEKKNVDQASGVSLLHLEVDGQVWLQVYGDGHDNG 226
Qy 227 LHGDHORESTAGLLP 243
Dy 227 LYADNVNDSTFTGFLLY 243

RESULT 7
ID APML_HUMAN STANDARD; PRT; 244 AA.
AC Q15848;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adiponectin precursor (30 kDa adipocyte complement-related protein)
DE (ACRP30) (Adipose most abundant gene transcript 1) (apM-1) (gelatin-
DE binding protein).
GN APM1 OR ACRP30 OR GBP28.
OS Homo sapiens (Human).
```

RA Yasaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y.,
 RA Kimura S., Tomita M., Kimura S., Ito C., Froguet P., Kadowaki T.;
 RT "Genetic variation in the gene encoding adiponectin is associated with
 an increased risk of type 2 diabetes in the Japanese population.";
 RL Diabetes 51:536-540(2002).
 CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE
 CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH
 CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING
 CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED
 CC EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE
 CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
 CC -1- SUBUNIT: HOMODIGLIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.
 CC -1- DISEASE: Defects in AP1 are the cause of adiponectin deficiency,
 CC resulting in very low concentration of plasma adiponectin.
 CC Decreased adiponectin plasma levels are associated with obesity
 CC insulin resistance, and diabetes type 2.
 CC -1- PHARMACEUTICAL: Adiponectin might be used in the treatment of
 CC diabetes type 2 and insulin resistance.
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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 CC -----
 DR EMBL; D45371; BAA08227.1; .
 DR EMBL; AB012165; BAA86716.1; .
 DR EMBL; AB012164; BAA86716.1; JOINED.
 DR EMBL; AJ131460; CAB52413.1; .
 DR EMBL; AJ131461; CAB52413.1; JOINED.
 DR MIM; 605441; .
 DR InterPro; IPR001073; Clq.
 DR InterPro; IPR000087; Collagen.
 DR Pfam; PF00386; Clq; 1.
 DR Pfam; PF01391; Collagen; 1.
 DR PRINTS; PR00007; COMPLEMENTC1Q.
 DR SMART; PS01110; Clq; 1.
 DR SMART; PS01113; Clq; 1.
 DR Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;
 KW Polymorphism; Disease mutation; Obesity; Diabetes mellitus.
 FT SIGNAL 1 14 POTENTIAL.
 FT CHAIN 15 244 ADIPONECTIN.
 FT DOMAIN 42 107 COLLAGEN-LIKE.
 FT DISULFID 36 36 INTERCHAIN (BY SIMILARITY).
 FT MOD_RES 44 44 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 47 47 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 53 53 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 62 62 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 71 71 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 76 76 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 86 86 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 95 95 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
 FT VARIANT 84 84 G -> R.
 FT VARIANT 112 112 /FTid=VAR_013273.
 FT VARIANT 117 117 R -> C (IN ADIPONECTIN DEFICIENCY).
 FT VARIANT 117 117 /FTid=VAR_013274.
 FT VARIANT 164 164 V -> M.
 FT VARIANT 164 164 /FTid=VAR_013275.
 FT VARIANT 221 221 I -> T.
 FT VARIANT 221 221 R -> S.
 FT VARIANT 241 241 /FTid=VAR_013276.
 FT VARIANT 241 241 R -> P.
 FT VARIANT 241 241 H -> P.
 FT SEQUENCE 244 AA; 26414 MW; 64D8C6C1204B1018 CRC64;

Query Match 21.5%; Score 293.5; DB 1; Length 244;
 Best Local Similarity 34.5%; Pred. No. 7.1e-18;
 Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;
 QY 53 QGP-----PGPPGP-----PGIPGNHGNNGNATGHEGAKGERGKGD---LGRP---GE 97
 Db 23 QGPGVLLPLPKGACTGWMAGIPGPHGNGAPGRDGTPEKGEKGDGPGIGPKGDIGE 82
 QY 98 RGQHGPKGEKGYGFI-----PPE-----LQIAPMASLATHFSNQNSGIIIFSSVETNIGNF 147
 Db 83 TGVPGAEGPRGFGIOGRKGEPEGAYVYRFAFSVGLTYVTIPNMPDRTKIFYNOONH 142
 QY 148 FDMVTGFGAPVSGVYFETFSMAKHDEVEVYVLMHNGNTVFSMYEYMKGRSDTSSNH 207
 Db 143 YDSTGKFKHCNIGLYFYFAHYIIVY--MKDVKVSFLFKDKAMLFYDQYQENNVDAQSGS 200
 QY 208 AVILKAKGDEWILRM-GNG---ALHGDHQRFTSFAGFLF 243
 Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLY 240
 RESULT 8
 CQT6_HUMAN STANDARD; PRT; 278 AA.
 ID CQT6_HUMAN
 AC Q9BXI9;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Complement-clq tumor necrosis factor-related protein 6 precursor.
 GN C1QTNF6 OR CTRP6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Piddington C.S., Sheppard P.O.;
 RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Tissue=Placenta;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AF329842; AAK17966.1; .
 DR EMBL; BC020551; AAK20551.1; .
 DR Genew; HGNC:14343; C1QTNF6.
 DR InterPro; IPR001073; Clq.
 DR InterPro; IPR000087; Collagen.
 DR Pfam; PF00386; Clq; 1.
 DR Pfam; PF01391; Collagen; 1.
 DR PRINTS; PR00007; COMPLEMENTC1Q.
 DR SMART; SM01110; Clq; 1.
 DR PROSITE; PS01113; Clq; FALSE_NEG.
 KW Collagen; Signal.
 FT SIGNAL 1 46 POTENTIAL.
 FT CHAIN 47 278 COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
 FT DOMAIN 97 138 RELATED PROTEIN 6.
 FT DOMAIN 139 278 COLLAGEN-LIKE.
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CONFLICT 21 21 G -> V (IN REF. 2).
SQ SEQUENCE 278 AA; 30861 MW; 27A82CA863F23D47 CRC64;

Query Match 21.2%; Score 289.5; DB 1; Length 278;
Best Local Similarity 28.8%; Pred. No. 1.8e-17;
Matches 78; Conservative 34; Mismatches 96; Indels 63; Gaps 10;

QY 9 WQLALFELFCODEYMESPTGGLPPDCSKC-----
Db 29 WAALLLFL--WCEIPWELTDRVASQCRCOCSEDLDPAHVSSASSSRPHALPE 85
QY 49 FRGY-----QGPFGPPGPIGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHG 102
Db 86 IRPVINITILKDGKDPGPNGLPGYMGREGPGQPGQSGKD-----
QY 103 PKGEGVPGIPPELQAFMA-----SLATHFSNQNGSIIFSSVETNIGNFDDVMTGRFGA 157
Db 129 -KGEMSGPAP--CQRFFAFSGVGRKTAHSGEDFOTLLFERVFNLDGCFDMATGQFAA 185
QY 158 PVSQVYFFTFPMKHIE-DVEEVVYVLMHNGNTVFSMYSYEMKCKSDTSSNHAVLKLAGD 216
Db 186 PLRGIYFFSLNV--HSNNYKETVHTMHNOKEAVILYA-OPSERSIQSQSVMLDLAYGD 242
QY 217 EVNLRM-----GNGALHGDHQRSTFAGFL 242
Db 243 RVVWRLFKRQRENAIYSNDFDTVTTFSGHLI 273

RESULT 9
GLIC_MOUSE
ID GLIC_MOUSE STANDARD; PRT: 255 AA.
AC Q9ESN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gliacolin precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA MEDLINE=20428709; PubMed=10862616;
RX Koide T., Aso A., Yorihuzi T., Nagata K.;
RT "Conformational requirements of collagenous peptides for recognition
RL J. Biol. Chem. 275:27957-27963(2000).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN GLIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; AB044560; BAB15806.1; -
DR InterPro; IPR001073; C1q.
DR pfam; PF00386; C1q; 1.
DR PRINTS; PR00007; Collagen; 1.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Collagen; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 255 GLIACOLIN.
FT DOMAIN 61 111 COLLAGEN-LIKE.
FT DOMAIN 120 255 C1Q.
SQ SEQUENCE 255 AA; 26687 MW; 529FBAF4B2191BC1 CRC64;

Query Match 20.9%; Score 285.5; DB 1; Length 255;
Best Local Similarity 34.2%; Pred. No. 3.5e-17;
Matches 68; Conservative 32; Mismatches 82; Indels 17; Gaps 5;

QY 61 PPOIPNHNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYGPIPELQIAF 120
Db 56 PTFIQPKGEAGRPGKAGPRGPPGPGPGVGPCKEKGPGRQGLPPGP-APGLNAAG 114
QY 121 MASLATH-----FSNQNSG---IIFSSVETNIGNFDVMTGRGAPVSGVYFFT 166
Db 115 AISAATYSTVPKIAFYAGLKRGHEVYELKFDVVTNLGNHNDPTTKGFTCSIPGIYFT 174
QY 167 FS-MKKHDEVEEVYVLMHNGNTVFSMYSYEMKCKSDTSSNHAVLKLAGDEVLMRNG 225
Db 175 YHVLMRGGDGTSMWADLCKNNQVRASAIQAQDADQNDYASNSVVLHLEPGDEVYIKLDG 234
QY 226 ALH-GDHQRSTFAGFLF 243
Db 235 KAHGNNKYSTFSGFIIY 253

RESULT 10
CALA_CHICK
ID CALA_CHICK STANDARD; PRT: 674 AA.
AC P08125;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Collagen alpha 1(X) chain precursor.
GN COL10A1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RA MEDLINE=48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466.
RX MEDLINE=8616822; PubMed=3082876;
RA Ninomiya Y., Gordon M., van der Rest M., Schmid T., Linsenmayer T.,
RA Olsen B.R.;
RT "The developmentally regulated type X collagen gene contains a long
RL open reading frame without introns.";
RL J. Biol. Chem. 261:5041-5050(1986).
RN [2]
RX MEDLINE=89054019; PubMed=2461368;
RA Luvallie P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;
RT "The type X collagen gene. Intron sequences split the 5'-untranslated
RT region and separate the coding regions for the non-collagenous amino-
RT terminal and triple-helical domains.";
RL J. Biol. Chem. 263:18378-18385(1988).
RN [3]
RA MEDLINE=89380199; PubMed=2476437;
RA Yanaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;
RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs
RT demonstrate that type VIII collagen is a short chain collagen and
RT contains triple-helical and carboxyl-terminal non-triple-helical
RT domains similar to those of type X collagen.";
RL J. Biol. Chem. 264:16022-16029(1989).
CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VII COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC
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FT CONFLICT 500 H -> L (IN REF. 3).
FT CONFLICT 567 A -> C (IN REF. 3).
FT CONFLICT 569 I -> H (IN REF. 3).
FT CONFLICT 571 FD -> IV (IN REF. 3).
FT CONFLICT 635 Q -> T (IN REF. 3).
SQ SEQUENCE 680 AA; 66775 MW; FE984CA99AF708E2 CRC64;

Query Match      20.4%; Score 278.5; DB 1; Length 680;
Best Local Similarity 30.5%; Pred. No. 4.1e-16;
Matches 73; Conservative 34; Mismatches 87; Indels 45; Gaps 7;

QY 45 GDYSFRGQGPPGPPIPCIPGNHNGNNGATG-----HEGAKEKDGKDGLGRGERG 99
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 443 CGPGIGTRGTPGPCVGFPGSGKDPNPAGPAGIATKGLTGNGPTGPPGPPGPRGHSG 502
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 100 QHGPKGEKGYGPIP-----PELQ-----IAFMASLATHF 128
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 503 EPLGEPGPPGPPGQAQVMPDGIKAGQRPLSGMPLVSANHVGTGMPVSAFTVLISKAY 562
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 129 SNQNSGIIFSSVETWIGNFDFVMTGRECAPGVSYVEFFFSMKKHEDVEEVYLMHNGNT 188
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 563 PAVGAPIFDDELYNRQHYPDRSIFTKPIGYTFSIHV--HKVGTHVMWGKYKNKTP 620
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 169 VFSMSYE--MWKGSDDTSNHAVKLAKGDEVWLRMGN---GALHGDHQRFSTAGFL 242
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 621 --TWITYDSKGYLDQAGSAINBELTENDQWLQLPNAESNGLYSSEYVHSFGFLV 677
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 12
CALA_BOVIN
ID CALA_BOVIN STANDARD; PRT; 674 AA.
AC P23206;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Collagen alpha 1(X) chain precursor.
GN COL10A1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA MEDLINE=9113131; Pubmed=1703407;
RA Thomas J.T., Kwan A.P.L., Grant M.E.; Boot-Handford R.P.;
RT "Isolation of cDNAs encoding the complete sequence of bovine type X
RT collagen. Evidence for the condensed nature of mammalian type X
RT collagen genes".
RL Blocham, J. 273:141-148(1991).
CC CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CC CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC CC -1- SUBUNIT: HOMOTRIMER.
CC CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC CC -1- SIMILARITY: CONTAINS 1 CIQ DOMAIN.
-----
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-----
DB EMBL; X53556; CAA37624.1; -.
DB PIR; S13301; S13301.
DB InterPro; IPR001073; Clq.
DB InterPro; IPR000087; Collagen.
DB Pfam; PF00386; Clq; 1.

```


Db 537 TPLVSNQGVTPMPVSAFTVILSKAYPAICTPIPEDKILYNROQHYDPRGTGFTQCPGI 596

QY 163 YPFTFSMMKHEDVEEVYVILMHNGNTVFSMYSYEMKGSDTSSNHAHLAKLAKGDEVLMRM 222

Db 597 YPFSYHV--HVKGTHVMGLKNGTPTVMTYDEYTKGYLDQASGSAIDLITENDQVWLQL 654

QY 223 GN--GALHGDHOREFTEAGFL 242

Db 655 PNAESNGLYSSEYVHSFSGFLV 677

RESULT 15

COT5_HUMAN

ID COT5_HUMAN STANDARD; PRT; 243 AA.

AC Q9BXJ0; Q9UFK4;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Complement-clq tumor necrosis factor-related protein 5 precursor.

GN C1QTNF5 OR CTRP5

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Sheppard P.O., Humes J.M.;

RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 25-243 FROM N.A.

RC TISSUE=Uterus;

RA Ottenwaelder B., Obermaier B., Mewes H.-W., Gassenhuber J.,

RA Wiemann S.;

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

CC -----

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CC -----

DR EMBL; AF329841; AAK17965.1; -.

DR EMBL; AL110261; CAB53702.1; -.

DR Genew; HGNC:14344; C1QTNF5.

DR InterPro; IPR001073; C1Q.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF00386; C1Q; 1.

DR Pfam; PF01391; Collagen; 1.

DR PRINTS; PR00007; COMPLEMENTC1Q.

DR SMART; SM01110; C1Q; 1.

DR PROSITE; PS01113; C1Q; FALSE_NEG.

KW Collagen; Signal.

FT SIGNAL 1 15 POTENTIAL.

FT CHAIN 16 243 COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-

FT 16 243 RELATED PROTEIN 5.

FT DOMAIN 30 95 COLLAGEN-LIKE.

FT DOMAIN 97 243 C1Q.

SQ SEQUENCE 243 AA; 25298 MW; 7CCDA65CDA7EB784 CRC64;

Query Match 19.3%; Score 264.5; DB 1; Length 243;

Best Local Similarity 32.6%; Pred. No. 2e-15;

Matches 74; Conservative 35; Mismatches 93; Indels 25; Gaps 9;

QY 34 GLPP-DCSK--CCHGDYSFRGYGPPGPPGPGIPGNHGNNGNNGATGHEGAKG--- 85

Db 15 GSPFLDNKTIPLCPG---HPGLPTFGHGSQGLFGRDGRDGRDGPAPGKEGGRP 71

QY 86 --KDGKDLGRGERGQHGPKEGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETN 143

Db 72 GLPGRGDPGPRCEAGPAGPTGPGAGCSVPPRSFAFSAKRSESRVPPSPDAPLPFDRVLVN 131

QY 144 IGNFDDMTGRFGAPVSGVYFFTFSSMMKHEDVEEVYV--LMHNGNTVFSMYSYEMKG-- 199

Db 132 EQGHYDAVTGKFTCQVPGVYFAV---HATVYRASLQFDLVKNGESIASFFQF-FGGWP 186

QY 200 KSDTSSNHAHLAKLAKGDEVLMRMNG--ALHGDHOREFTEAGFL 243

Db 187 KPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTIDSTFSGLVY 233

Search completed: January 13, 2003, 10:43:07

Job time : 14 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2003, 10:41:03 ; Search time 33 Seconds
(without alignments)
1535.988 Million cell updates/sec

Title: -US-09-931-836-2

Perfect score: 1367

Sequence: 1 MLWRQLIYWQLLALFLPFC.....LHGDKRSTFAGLLFETK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rhodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1311	95.9	246	11 Q9ES30	Q9es30 mus musculus
2	313	22.9	294	11 Q9B8U4	Q9b8u4 mus musculus
3	299	21.9	240	6 Q95M04	Q95mq4 bos taurus
4	293.5	21.5	243	6 Q95JD7	Q95jd7 macaca mula
5	276.5	20.2	675	6 Q9N178	Q9n178 sus scrofa
6	273	20.0	1077	4 Q8TE71	Q8te71 homo sapien
7	270	19.8	295	11 Q9Z1K4	Q9z1k4 rattus norv
8	266.5	19.5	158	4 Q9H667	Q9h667 homo sapien
9	258.5	18.9	705	4 Q8TE75	Q8te75 homo sapien
10	257.5	18.8	243	11 Q8R002	Q8r002 mus musculus
11	257.5	18.8	744	4 Q96D07	Q96d07 mus musculus
12	257	18.8	744	11 Q9B2V4	Q9b2v4 mus musculus
13	257	18.8	744	11 Q9Z1S8	Q9z1s8 mus musculus
14	247.5	18.1	194	6 Q95J95	Q95j95 canis famil
15	239.5	17.5	245	11 Q9DCM6	Q9dcm6 mus musculus
16	237.5	17.4	281	11 Q9QXP7	Q9qxp7 mus musculus

17	219.5	16.1	347	4 Q96IH6	Q96ih6 homo sapien
18	218	15.9	1017	11 Q99KA1	Q99ka1 mus musculus
19	216	15.8	2944	11 Q63870	Q63870 mus musculus
20	215	15.7	583	4 Q96G58	Q96g58 homo sapien
21	215	15.7	992	4 Q9UG76	Q9ug76 homo sapien
22	215	15.7	1016	4 Q9Y6C2	Q9y6c2 homo sapien
23	211	15.4	182	11 Q8R1P2	Q8r1p2 mus musculus
24	210.5	15.4	422	5 Q24893	Q24893 ephydatia m
25	207.5	15.2	1549	11 Q60444	Q60444 cricetus
26	203.5	14.9	673	4 Q14052	Q14052 homo sapien
27	197	14.4	171	13 Q90S86	Q90s86 gallus gall
28	195.5	14.3	1140	11 Q61434	Q61434 mus musculus
29	195.5	14.3	1774	11 Q62001	Q62001 mus musculus
30	194	14.2	224	5 Q9VVY2	Q9vvv2 drosophila
31	194	14.2	397	16 Q8XLT5	Q8xlt5 clostridium
32	191.5	14.0	594	5 Q9VEP4	Q9vep4 drosophila
33	190.5	13.9	289	5 Q62432	Q62432 caenorhabdi
34	190.5	13.9	890	5 Q77087	Q77087 alvinella p
35	190	13.9	476	13 Q918D5	Q918d5 gallus gall
36	189	13.8	292	11 Q9CS87	Q9csb7 mus musculus
37	189	13.8	375	4 Q8TCD8	Q8tcd8 homo sapien
38	188.5	13.8	187	11 Q9JHA9	Q9jha9 rattus norv
39	188.5	13.8	1745	4 Q9NZ06	Q9nzz6 homo sapien
40	188	13.8	1344	13 Q93419	Q93419 gallus gall
41	187.5	13.7	680	11 Q9D0D2	Q9d0d2 mus musculus
42	185.5	13.6	303	5 Q23364	Q23364 caenorhabdi
43	185.5	13.6	1723	5 Q9G0B1	Q9gqb1 hydra atten
44	185	13.5	408	13 Q90604	Q90604 gallus gall
45	185	13.5	441	4 Q96A84	Q96a84 homo sapien

ALIGNMENTS

RESULT 1

Q9ES30	PRELIMINARY;	PRT;	246 AA.
AC Q9ES30			
DT 01-MAR-2001 (TrEMBLrel. 16, Created)			
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DE Collageneous repeat-containing sequence of 26kda protein.			
DE Collageneous repeat-containing sequence of 26kda protein.			
GN COR5 OR COR526..			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-21264842; PubMed-11071891;			
RA Maeda T., Abe M., Kurisu K., Jikko A., Furukawa S.;			
RT "Molecular cloning and characterization of a novel gene, COR526,			
RT encoding a putative secretory protein and its possible involvement in			
RT skeletal development."			
RL J. Biol. Chem. 276:3628-3634(2001).			
DR EMBL: AF246265; AAC33704.1; -;			
DR MGD; MGI:1932136; Cors.			
DR InterPro; IPR001073; Clq.			
DR InterPro; IPR000087; Collagen.			
DR Pfam; PF00386; Clq; 1.			
DR Pfam; PF01391; Collagen; 1.			
DR PRINTS; PRO0007; COMPLEMENTC1Q.			
DR SMART; SM00110; Clq; 1.			
DR PROSITE; PS01113; Clq; 1.			
SQ SEQUENCE 246 AA; 26828 MW; 42A481B3E9F48F7E CRC64;			

Query Match 95.9%; Score 1311; DB 11; Length 246;

Best Local Similarity 95.9%; Pred No. 9.2e-110;

Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MLWRQLIYWQLLALFLPFCODEYMESPTGGLPDCSKCHGDSYFRGQGGPPPG 60

DB 1 MLGRQRIWHLPLFLPFCODEYMESPTGGLPDCSKCHGDSYFRGQGGPPPG 60

```
QY 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGQHGPKGKGYGPIPELQIAF 120
Db 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGQHGPKGKGYGPIPELQIAF 120
QY 121 MASLATHFSNQSGIIFSSVETNIGNFDVMTGRCAPVSGVYFFTFSMKHEDVEEYIV 180
Db 121 MASLATHFSNQSGIIFSSVETNIGNFDVMTGRCAPVSGVYFFTFSMKHEDVEEYIV 180
QY 181 YLMHNGNTVFSYMYEMKSDTSSNAVLKAKGDEWLRMGALHGDHQRSTFAGF 240
Db 181 YLMHNGNTVFSYMYETKSDTSSNAVLKAKGDEWLRMGALHGDHQRSTFAGF 240
QY 241 LLETK 246
Db 241 LLETK 246

RESULT 2
Q9D8U4 PRELIMINARY; PRT; 294 AA.
ID Q9D8U4 AC Q9D8U4
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1810033K05RIK protein.
GN 1810033K05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007683; BAB25187.1; -.
DR MGD: MGI:1916433; 1810033K05RIK.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Clq.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 2.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
DR SEQUENCE 294 AA; 30865 MW; 6D3905AE7C19E6FA CRC64;

Query Match 22.9%; Score 313; DB 11; Length 294;
Best Local Similarity 28.9%; Pred. No. 3.8e-20;
Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;

QY 6 LIYWQLLALFFPLFCODEYN-----ESPQTGLPPDCSKCHGDSFRGYQGPGPP 59
Db 10 MISWILLAC-ALP---CAADPMGLAFARDFKGGPQLVCS-----LPGPQGP 54
```

```
QY 60 GPGIPGNHNGNNGATGHEGAKGKDGKDG-----L 92
Db 55 GPPAPGSSGVVGRMGPPGKDGQGDGSDGEBEPPGRTGNRGKQGPKGAGAIIRA 114
QY 93 GPRGR-----GQHPKPKGKGYGPIP-----PELQIAPMASLATHFSNQNS 133
Db 115 GPRGPKVSGTPGKHGTPGKKGPKGKKGPELPGPCSCGSSRAKSAFSVAVTKSYPERL 174
QY 134 GIIFSSVETNIGNFDVMTGRCAPVSGVYFFTFSMK---KHEDVEEYVYLMHNGNTVF 190
Db 175 PIKDKILMNEGGHYNASSGRKFCVSGPIIYFTIIDLANKH-----LAIGLVHNGQ--Y 227
QY 191 SMYSYEMK-GKSDTSSNAVLKAKGDEWLRM-----GNGLAGHDHQRSTFAGFLF 243
Db 228 RIRFDANTGNHDVAGSSTILALKEGDEVWLQIFYSEQNGLFYDPYWTDSILFTGLIY 285

RESULT 3
Q95M04 PRELIMINARY; PRT; 240 AA.
ID Q95M04 AC Q95M04
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adipose tissue-specific protein adipo Q.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21369933; PubMed=11382781;
RA Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;
RT "Identification and Adipocyte Differentiation-dependent Expression of
RT the Unique Disialic Acid Residue in an Adipose Tissue-specific
RT Glycoprotein, Adipo Q.";
RL J. Biol. Chem. 276:28849-28856(2001).
DR EMBL: AF269230; AAK58902.1; -.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 1.
DR ProDom: PD000007; Collagen; 1.
DR PROSITE: PS01113; C1Q; UNKNOWN.1.
DR SEQUENCE 240 AA; 26091 MW; C6253BA803B9A668 CRC64;

Query Match 21.9%; Score 299; DB 6; Length 240;
Best Local Similarity 33.3%; Pred. No. 5.4e-19;
Matches 75; Conservative 35; Mismatches 85; Indels 30; Gaps 7;

QY 44 HGDSYFRGQGGPPGPP-----PGIPGNHNGNNGATGHEGAKGKDGKDG---LGPR 95
Db 16 HGEDNM---EDPLPKGACAGWMAGIPGPHGNGTTPGRDGRDTPGKEGKDGAGLLGPK 72
QY 96 GER---GQHPKPKGKGYGPIPE-----LQIAFNASLATHFSNQNSGIIFSSVET 142
Db 73 GETGDVGMTGAEGPPGPGTGRKKGPEGRAAYVYRFAVSVGLETRVTVNVPPIRFTKIFY 132
QY 143 NIGNEFDVMTGRCAPVSGVYFFTFSMKHEDVEEYVYLMHNGNTVFSYMYEMKGDSD 202
Db 133 NQNHVDGSGTGKFCYCNIPGLYFYSYHITVY--MKDKVSLFKKDKAVLEFTYDQYQKNVD 190
QY 203 TSSNAHVLKAKGDEWLRMGALH-----GDHQRSTFAGFLF 243
Db 191 QASGVLLHLEVDGVWLQVYEGENHNGVYADNVNDSTFTGFLLY 235

RESULT 4
Q95JD7 PRELIMINARY; PRT; 243 AA.
ID Q95JD7 AC Q95JD7
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DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Adiponectin.
GN	APM1.
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=ADIPOSE TISSUE;
RX	MEDLINE=21232234; PubMed=11334417;
RA	Hotta K., Funahashi T., Bockin N.L., Ortmeier H.K., Arita Y.,
RA	Hansen B.C., Matsuzawa Y.;
RT	*Circulating concentrations of the adipocyte protein adiponectin are
RT	decreased in parallel with reduced insulin sensitivity during the
RT	progression to type 2 diabetes in rhesus monkeys.;
RL	Diabetes 50:1126-1133(2001).
DR	EMBL; AF0404407; AAK92202.1; -.
DR	InterPro; IPR001073; Clq.
DR	InterPro; IPR000087; Collagen.
DR	Pfam; PF00386; Clq; 1.
DR	Pfam; PF01391; Collagen; 1.
DR	ProDom; PD000007; Collagen; 1.
DR	PROSITE; PS01113; ClQ; UNKNOWN_1.
SQ	SEQUENCE 243 AA; 26264 MW; 49A45DAF2B4613FD CRC64;
Query Match	
Best Local Similarity 31.5%; Score 293.5; DB 6; Length 243;	
Matches 75; Conservative 37; Mismatches 77; Indels 31; Gaps	
Qy	53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGEKDGKD---LGPRGERGQ 100
Db	22 QCGVGLPLPKGACTGWMAGIPHPGNGVPGRDGRDGTPEKGEKGDPLGLGPKGDTGE 81
Qy	101 ---HGPKGEKGYPGI-----PPP-----LQIAFMASLATHFNSNONSGLIFFSVETNIGNF 147
Db	82 TGVTAGSGRPGFGPIQGRKGEPCGEGAVVYRSASVGLGTVTVPNPIRTKIFYNQNH 141
Qy	148 FDMVTGRFGAPVSCVYFTFSMKKHEDVEEYVYLHMNGNTVFSYEMKMGKSDTSSNH 207
Db	142 YDGTGTFHGNIPGLYFYFAYHIYTV--MKDVKVSLFKKAMLFYDQYQENNVDQASGS 199
Qy	208 AVLKAKRGDQVWLMRM--GNG---ALHGDHQRFSTFAGFLLF 243
Db	200 VLLHLEVGDDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 239
RESULT 5	
Q9N178	PRELIMINARY; PRT; 675 AA.
ID	Q9N178
AC	Q9N178;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Type x collagen.
GN	COL10A1.
OS	Sus scrofa (pig).
OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21015405; PubMed=11130976;
RA	Nielsen V.H., Bendixen C., Arnbjerg J., Sorensen C.M., Jensen H.E.,
RA	Shukri N.M., Thomsen B.;
RT	*Abnormal growth plate function in pigs carrying a dominant mutation
RT	in type x collagen.;
RL	Mamm. Genome 11:1087-1092(2000).
DR	EMBL; AF222861; AAF37271.1; -.
DR	InterPro; IPR001073; Clq.


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QY 99 GQHGPKGKGYGPGIP-----PELQI-----AFM 121
Db 521 GPPCPGPPGAPGAFDEGTAGLHLPNGCVGAVLKGGRPQFGLGELSAHATPAET 580
QY 122 ASLATHFSNQNSGIFFSVETNIGNFDMVTGREGAPVSGVYFFTFSMKHEDVEEVYV 181
Db 581 AVLTSPFPASGMPVKFDTLYNGHSGYNPATGIFTCPVGGVYFAY-----HVVHVKGTNVW 636
QY 182 LMHNGNTVFSMYSVE--MKCKSDTSSNHAVLKLAKGDEVWLRM-----GNCALHGDHQRFS 235
Db 637 VALYKNNVPATYTYDEYKKGYLDOAGGAVLQLRPNQVWVQMPDQANG-LYSTVEIHS 695
QY 236 TFAGFLFET 245
Db 696 SFSGFLLCPT 705

RESULT 10
Q8R002 ID Q8R002 PRELIMINARY; PRT; 243 AA.
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
OS Similar to DKFZP386B0621 protein (Hypothetical 25.4 kDa protein).
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023068; AAH23068.1; -.
DR EMBL; BC025174; AAH25174.1; -.
KW Hypothetical protein.
SQ SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;

Query Match 18.8%; Score 257.5; DB 11; Length 243;
Best Local Similarity 32.58%; Pred. No. 2.9e-15;
Matches 81; Conservative 33; Mismatches 100; Indels 35; Gaps 10;

QY 11 LLALFFLPCLCQDEYME$PQTGGLPDCSK---CCHGDYSFRGVQGPVPPGPGIPGN 67
Db 4 LLALLLLGLV-----SGSPPLDDNKIPSLCPQ---PGLPGTPHHGSGQLPGR 49
QY 68 HCNNGNNGATGHEGAKGKDGKGLGPRGE---RQHGPKGKGYGPG---IPPELQIAFM 121
Db 50 DGRDGRDGAAPGAPGKGGCGRPLGPRGEPGRGEAGPMCAIGPAGECSVPPPSAFSAK 109
QY 122 ASLATHFSNQNSGIFFSVETNIGNFDMVTGREGAPVSGVYFFTFSMKHEDVEEVYV 181
Db 110 RSESRVPPADTLPFDRVLLNEOGHEDPTTKETQCVQGVYFAY-----HATVYRASLQ 165
QY 182 --LMHNGNTVFSMYSYEMKG--KSDTSSNHAVLKLAKGDEVWLRMNG---ALHGDHQR 234
Db 166 FDLVKNQGSIA$FFQY-FGGWPKPASLGGAMVRLPEQDQVWVQGVGDIGIYASIKTD 224
QY 235 TFAGFLFET 243
Db 225 STFSGFLVY 233

RESULT 11
Q96D07 ID Q96D07 PRELIMINARY; PRT; 744 AA.
AC Q96D07
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
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DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 73.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013581; AAH13581.1; -.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 7.
DR ProDom; PD000007; Collagen; 2.
DR ProSITE; PS01113; Clq; UNKNOWN_1.
KW Collagen; Hypothetical protein.
SQ SEQUENCE 744 AA; 73364 MW; 2BC1B0955DE2C9A3 CRC64;

Query Match 18.8%; Score 257.5; DB 4; Length 744;
Best Local Similarity 29.98%; Pred. No. 1.1e-14;
Matches 78; Conservative 26; Mismatches 102; Indels 55; Gaps 6;

QY 34 GLPPDCSKCHDYSFRGVQGPVPPGPGIPGNHNGNG-----NNGATGHEGAKGE 85
Db 486 GIPGD--QGLGPGIPGIGGPGIPGPGIPGPGKPGPLGPGPGPGPGVAGLHP 543
QY 86 KGDKGLGPRGCHGPKGKGYGPGIP-----PELQI----- 118
Db 544 PKGPGALGPQCQGLPGLGPGPGPGPGVPPPPQGEYLPDMGLGIDGVKPPHAYGA 603
QY 119 -----AFMASLATHFSNQNSGIFFSVETNIGNFDMVTGREGAPVSGVYEF 165
Db 604 KKGNGGPAVEPAFTAELTAPPVPCAPVKFNKLLNGRQNYNPQTGTCFCEVPGVYIF 663
QY 166 TFSMKHEDVEEVYVLMHNGNTVFSYEMKSKDSTSSNHAVLKLAKGDEVWLRMNG- 224
Db 664 AYHV--HCKGNNVWVAFKKNPEYTYDEYKKGFLDOAGSAVLLLRPGDRVFLQMPSE 721
QY 225 --GALHGDHQRFS$TFAGFLLF 243
Db 722 QAAGLYAGQVH$SFSGYLLY 742

RESULT 12
Q9D2V4 ID Q9D2V4 PRELIMINARY; PRT; 744 AA.
AC Q9D2V4
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE Procollagen, type VIII, alpha 1.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kasaiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King H., Sacchi V.,
RA Kuehl P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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[illegible]

Query Match	17.5%;	Score 239.5;	DB 11;	Length 245;
Best Local Similarity	33.2%;	Preid. No. 1.2e-13;		
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31	KGKAGCNPGRPGRLKGERPEGAAGIRTGIRFGKDGPGESGPPCKPGNVGLPPGSPG 90			
95	RGRGQHGPKEGKGYPG-IPPELQIAFMASLATHEFSNQNSGIFFSSVETNIGNFEDVMTG 153			
91	LGDSPGQGLKGVKNGPNTRDQRPRAEFAIRQNPMTLGNV-VIEDKVLTKQESPYNHTC 149			
154	REGAPYSGVVFFETFSMMKHEDVEEYVYVLMHNG--NTVFSMYSTEMGKSDTSNNHAYLK 211			
150	RFTCANVPGYFFNFQVSKWDL-:CIFIKSSSGGQPRDLSFSFNTNNRGLFQVLAGGTGLQ 208			

7:

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:42:54 ; Search time 10 Seconds
(without alignments)
477.266 Million cell updates/sec

Title: US-09-931-836-2

Perfect score: 1367

Sequence: 1 MLWRQLIYWQLLALFLPFC.....LHGDRHRETFAGLLFETK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	100.0	246	9	US-10-036-041-2
2	1367	100.0	246	12	US-10-036-342-2
3	294	21.5	247	10	US-09-776-976-4
4	294	21.5	247	10	US-09-758-055-4
5	294	21.5	247	10	US-09-909-547-4
6	293.5	21.5	244	9	US-09-911-1768-48
7	293.5	21.5	244	10	US-09-776-976-6
8	293.5	21.5	244	10	US-09-758-055-6
9	293.5	21.5	244	10	US-09-909-547-6
10	293	21.4	247	10	US-09-776-976-2
11	293	21.4	247	10	US-09-758-055-2
12	293	21.4	247	10	US-09-909-547-2
13	290.5	21.3	259	9	US-09-989-293A-47
14	290.5	21.3	259	9	US-09-989-735-47
15	290.5	21.3	259	9	US-09-989-730-47
16	290.5	21.3	259	9	US-09-989-730-47
17	290.5	21.3	259	9	US-09-989-730-47
18	290.5	21.3	259	9	US-09-989-730-47
19	290.5	21.3	259	9	US-09-991-181-47

20	290.5	21.3	259	9	US-09-993-687-47	Sequence 47, Appl
21	290.5	21.3	259	9	US-09-989-734-47	Sequence 47, Appl
22	290.5	21.3	259	10	US-09-989-722-47	Sequence 47, Appl
23	290.5	21.3	259	10	US-09-989-723-47	Sequence 47, Appl
24	290.5	21.3	259	10	US-09-989-279-47	Sequence 47, Appl
25	290.5	21.3	259	10	US-09-989-727-47	Sequence 47, Appl
26	290.5	21.3	259	10	US-09-989-731-47	Sequence 47, Appl
27	290.5	21.3	259	10	US-09-989-732-47	Sequence 47, Appl
28	290.5	21.3	259	10	US-09-991-073-47	Sequence 47, Appl
29	290.5	21.3	259	10	US-09-990-442-47	Sequence 47, Appl
30	290.5	21.3	259	10	US-09-991-163-47	Sequence 47, Appl
31	290.5	21.3	259	10	US-09-993-604-47	Sequence 47, Appl
32	290.5	21.3	259	10	US-09-990-456-47	Sequence 47, Appl
33	290.5	21.3	259	10	US-09-989-721-47	Sequence 47, Appl
34	290.5	21.3	259	12	US-10-052-586-62	Sequence 62, Appl
35	289.5	21.2	278	10	US-09-799-777-35	Sequence 35, Appl
36	287	21.0	247	9	US-09-911-1768-3	Sequence 3, Appl
37	273	20.0	746	9	US-09-854-133-185	Sequence 185, App
38	273	20.0	746	10	US-09-738-973-185	Sequence 185, App
39	264.5	19.3	243	9	US-09-944-413-42	Sequence 42, Appl
40	264.5	19.3	243	9	US-09-944-403-42	Sequence 42, Appl
41	264.5	19.3	243	9	US-09-944-896-42	Sequence 42, Appl
42	264.5	19.3	243	9	US-09-944-944-42	Sequence 42, Appl
43	264.5	19.3	243	9	US-09-944-907-42	Sequence 42, Appl
44	264.5	19.3	243	9	US-09-944-929-42	Sequence 42, Appl
45	264.5	19.3	243	9	US-10-028-072-362	Sequence 362, App

ALIGNMENTS

RESULT 1

US-10-036-041-2
; Sequence 2, Application US/10036041
; Publication No. US20020192751A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C8
; CURRENT APPLICATION NUMBER: US/10/036,041
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
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; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
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; PRIOR APPLICATION NUMBER: 60/135750
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; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
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; PRIOR APPLICATION NUMBER: 60/146970
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; PRIOR APPLICATION NUMBER: PCT/US99/28551
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; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-041-2

Query Match 100.0%; Score 1367; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. le-111; Indels 0; Gaps 0;
Matches 246; Conservative 0; Mismatches 0;

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Qy 181 YLMHNGNTVFSMYSYEMKGSKDTSSNHAVLKLAKEDEFWLGMNGALHGDHQRSTFAGF 240
Db 181 YLMHNGNTVFSMYSYEMKGSKDTSSNHAVLKLAKEDEFWLGMNGALHGDHQRSTFAGF 240
Qy 241 LLFETK 246
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RESULT 2
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; Sequence 2, Application US/10036342
; Patent No. US20020090681A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030RIC5
; CURRENT APPLICATION NUMBER: US/10/036,342
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
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; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131272
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-342-2

Query Match 100.0%; Score 1367; DB 12; Length 246;
Best Local Similarity 100.0%; Pred. No. 1e-111;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWRQLIYWQLLALFLPFLCQDEYMESPTGGLPDCSKCCCHGDSYFRGYGPPGPPG 60
Db 1 MLWRQLIYWQLLALFLPFLCQDEYMESPTGGLPDCSKCCCHGDSYFRGYGPPGPPG 60
Qy 61 PPGIPGNHNGNNGATGHEGAKGDKGDLGPRGERGOGHPKRGKYGPIPELQIAF 120
Db 61 PPGIPGNHNGNNGATGHEGAKGDKGDLGPRGERGOGHPKRGKYGPIPELQIAF 120
Qy 121 MASLATHFSNQNSGIIFFSVETNIGNFDYMTGRFAPVSGVYFFTFSMKHEDVEEYV 180
Db 121 MASLATHFSNQNSGIIFFSVETNIGNFDYMTGRFAPVSGVYFFTFSMKHEDVEEYV 180
Qy 181 YLMHNGNTVFSMYSEYEMKGSKSDTSSNHAVALKLAKGDEVLRMGNGALHGDHQRSTFAGF 240
Db 181 YLMHNGNTVFSMYSEYEMKGSKSDTSSNHAVALKLAKGDEVLRMGNGALHGDHQRSTFAGF 240
Qy 241 LLFETK 246
Db 241 LLFETK 246

RESULT 3
US-09-776-976-4
; Sequence 4, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.US4.REG
; CURRENT APPLICATION NUMBER: US/09/776,976
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087


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; Sequence 48, Application US/09911176B
; Patent No. US20020156243A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ANTIBODIES THAT BIND AN
; FILE REFERENCE: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
; CURRENT FILING DATE: 1997-07-18
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 1998-07-17
; PRIOR FILING DATE: 1998-07-17
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-176B-48

Query Match          21.5%; Score 293.5; DB 9; Length 244;
Best Local Similarity 34.5%; Pred. No. 1.7e-18;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKDGKGD---LGPR---GE 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGCHNGAPGRDGTTPGKEGKGDPLGPKGDIGE 82

QY 98 RGQHPKPKGKGYPGI-----PPE-----LQIAFMASLATHFSNQSGIIFSSVETNIGNF 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TGVPGAEGPRGPGIQRKGECEGAYVYRSFVGLTYVTIPNPIRFTKIFYNQNH 142

QY 148 FDMVTGRFGAPVSGVYFFTFSSMKKHEDVEVYVYLMHNGNTVFSYEMKCKSDTSSNH 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDGTGKFKHCNIPGLYFYFAYHTIVY--MKDVKVSFLFKDKKAMLFYDQYQENNVDAQSGS 200

QY 208 AVLKLAGDEWLRM-GNG---ALHGDHORFTFAGFLLF 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240

RESULT 7
US-09-776-976-6
; Sequence 6, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.USA.REG
; CURRENT FILING DATE: 2001-02-05
; PRIOR FILING DATE: 2001-01-10
; PRIOR FILING DATE: 2001-01-10
; PRIOR FILING DATE: 2000-01-14
; PRIOR FILING DATE: 2000-04-13
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-976-6

Query Match          21.5%; Score 293.5; DB 10; Length 244;
Best Local Similarity 34.5%; Pred. No. 1.7e-18;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKDGKGD---LGPR---GE 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGCHNGAPGRDGTTPGKEGKGDPLGPKGDIGE 82

QY 98 RGQHPKPKGKGYPGI-----PPE-----LQIAFMASLATHFSNQSGIIFSSVETNIGNF 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TGVPGAEGPRGPGIQRKGECEGAYVYRSFVGLTYVTIPNPIRFTKIFYNQNH 142

QY 148 FDMVTGRFGAPVSGVYFFTFSSMKKHEDVEVYVYLMHNGNTVFSYEMKCKSDTSSNH 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDGTGKFKHCNIPGLYFYFAYHTIVY--MKDVKVSFLFKDKKAMLFYDQYQENNVDAQSGS 200

QY 208 AVLKLAGDEWLRM-GNG---ALHGDHORFTFAGFLLF 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240

RESULT 9
US-09-909-547-6
; Sequence 6, Application US/09909547
; Patent No. US20020091080A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
US-09-909-547-6
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; Sequence 48, Application US/09911176B
; Patent No. US20020156243A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ANTIBODIES THAT BIND AN
; FILE REFERENCE: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
; CURRENT FILING DATE: 1997-07-18
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 1998-07-17
; PRIOR FILING DATE: 1998-07-17
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-176B-48

Query Match          21.5%; Score 293.5; DB 9; Length 244;
Best Local Similarity 34.5%; Pred. No. 1.7e-18;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKDGKGD---LGPR---GE 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGCHNGAPGRDGTTPGKEGKGDPLGPKGDIGE 82

QY 98 RGQHPKPKGKGYPGI-----PPE-----LQIAFMASLATHFSNQSGIIFSSVETNIGNF 147
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Db 83 TGVPGAEGPRGPGIQRKGECEGAYVYRSFVGLTYVTIPNPIRFTKIFYNQNH 142

QY 148 FDMVTGRFGAPVSGVYFFTFSSMKKHEDVEVYVYLMHNGNTVFSYEMKCKSDTSSNH 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDGTGKFKHCNIPGLYFYFAYHTIVY--MKDVKVSFLFKDKKAMLFYDQYQENNVDAQSGS 200

QY 208 AVLKLAGDEWLRM-GNG---ALHGDHORFTFAGFLLF 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240

RESULT 8
US-09-758-055-6
; Sequence 6, Application US/09758055
; Patent No. US20020058617A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.USA.REG
; CURRENT FILING DATE: 2001-01-10
; PRIOR FILING DATE: 2001-01-10
; PRIOR FILING DATE: 2000-01-14
; PRIOR FILING DATE: 2000-01-14
; PRIOR FILING DATE: 2000-04-13
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-055-6

Query Match          21.5%; Score 293.5; DB 10; Length 244;
Best Local Similarity 34.5%; Pred. No. 1.7e-18;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKDGKGD---LGPR---GE 97
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Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGCHNGAPGRDGTTPGKEGKGDPLGPKGDIGE 82

QY 98 RGQHPKPKGKGYPGI-----PPE-----LQIAFMASLATHFSNQSGIIFSSVETNIGNF 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TGVPGAEGPRGPGIQRKGECEGAYVYRSFVGLTYVTIPNPIRFTKIFYNQNH 142

QY 148 FDMVTGRFGAPVSGVYFFTFSSMKKHEDVEVYVYLMHNGNTVFSYEMKCKSDTSSNH 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDGTGKFKHCNIPGLYFYFAYHTIVY--MKDVKVSFLFKDKKAMLFYDQYQENNVDAQSGS 200

QY 208 AVLKLAGDEWLRM-GNG---ALHGDHORFTFAGFLLF 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240

RESULT 9
US-09-909-547-6
; Sequence 6, Application US/09909547
; Patent No. US20020091080A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
US-09-909-547-6
```

APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US6.CIP
CURRENT APPLICATION NUMBER: US/09/909,547
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 6
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-547-6

Query Match 21.5%; Score 293.5; DB 10; Length 244;
Best Local Similarity 34.5%; Pred. No. 1.7e-18;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;
Qy 53 QGP-----PGPGP-----PPE-----LQAFMASLATHFSNONGIIFSSVETNIGNF 97
Db 23 QGPGVLLPLPKGACTGMAGIPGPHGNGAPGRDGTGPKGKGDPLGPKGDIGE 82
Qy 98 RQHGPKGKGYGPGI-----PPE-----LQAFMASLATHFSNONGIIFSSVETNIGNF 147
Db 83 TCVPGAEGPRGPGIQRKGPEGGAYVYRSFSAFVGLTYTIPNMPITRKIFYNQNH 142
Qy 148 FDMWTGRGAPVSGVYFTFSMKHEDVEEYVYLMHNGNTVFSMYEMKGSKSDTSSNH 207
Db 143 YDGTGKFCNIPGLYFYHITVY--MKDKVSLFKKDKKAMLTYYDQYQENVDQASGS 200
Qy 208 AVLKAKGDEVWLRM-GNG-----ALHGDHOFSTFAGFLLF 243
Db 201 VLLHLEVDQWLQYGEGRNGLYADNDSTFTGFLLY 240

RESULT 10
US-09-776-976-2
Sequence 2, Application US/09776976
Patent No. US20020037849A1
GENERAL INFORMATION:
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 2
LENGTH: 247
TYPE: PRT
ORGANISM: mus musculus

US-09-776-976-2

Query Match 21.4%; Score 293; DB 10; Length 247;
Best Local Similarity 31.2%; Pred. No. 1.9e-18;
Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;
Qy 6 LIYWOLLALFPLCLCODEYMESPTGG--LPPDCSKCHGDYSFRGYQGPFGPPG 63
Db 2 LLLQALLFLLLP-SHAEDDDVTTEELAPALVPPPKGTCA-----GWMA-----G 45
Qy 64 IPGNHNGNNGATGHEGAKGKDGKD---LGRGER---GQHGPKGKGYGPPIPE-- 115
Db 46 IPGSHNGTFRDGRDGTGPKGKGDGSLGPKGTGDMGTGAGPRGFGPTGPKRG 105
Qy 116 -----LQAFMASLATHFSNONGIIFSSVETNIGNFDMTGRFAPVSGVYFTF 167
Db 106 EPGEAAVYVRSFVGLTRVTVPNVPIRFTKIFYNQNHYNSTGKFCYNIPGLIYFSY 165
Qy 168 SMKHEDEVYVYLMHNGNTVFSMYEMKGSKSDTSSNHAVLKLAKGDEVWLRM-GNG- 225
Db 166 HITVY--MKDKVSLFKKDKKAVLFTYDQYQENVDQASGSLHLEVDQWLQYVGDG 223
Qy 226 ---ALHGDHOFSTFAGFLLF 243
Db 224 HNGLYADNDSTFTGFLLF 243

RESULT 11
US-09-758-055-2
Sequence 2, Application US/09758055
Patent No. US20020058617A1
GENERAL INFORMATION:
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 2
LENGTH: 247
TYPE: PRT
ORGANISM: mus musculus
US-09-758-055-2

Query Match 21.4%; Score 293; DB 10; Length 247;
Best Local Similarity 31.2%; Pred. No. 1.9e-18;
Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;
Qy 6 LIYWOLLALFPLCLCODEYMESPTGG--LPPDCSKCHGDYSFRGYQGPFGPPG 63
Db 2 LLLQALLFLLLP-SHAEDDDVTTEELAPALVPPPKGTCA-----GWMA-----G 45
Qy 64 IPGNHNGNNGATGHEGAKGKDGKD---LGRGER---GQHGPKGKGYGPPIPE-- 115
Db 46 IPGSHNGTFRDGRDGTGPKGKGDGSLGPKGTGDMGTGAGPRGFGPTGPKRG 105
Qy 116 -----LQAFMASLATHFSNONGIIFSSVETNIGNFDMTGRFAPVSGVYFTF 167
Db 106 EPGEAAVYVRSFVGLTRVTVPNVPIRFTKIFYNQNHYNSTGKFCYNIPGLIYFSY 165
Qy 168 SMKHEDEVYVYLMHNGNTVFSMYEMKGSKSDTSSNHAVLKLAKGDEVWLRM-GNG- 225
Db 166 HITVY--MKDKVSLFKKDKKAVLFTYDQYQENVDQASGSLHLEVDQWLQYVGDG 223

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Qy 226 --ALHGDHQRSTFAGFLF 243
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Db 224 HNGLYADNVNDSTFTGFLF 243

RESULT 12
US-09-909-547-2
; Sequence 2, Application US/09909547
; Patent No. US20020091080A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.US6.CIP
; CURRENT APPLICATION NUMBER: US/09/909,547
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/176,228
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: mus musculus
US-09-909-547-2

Query Match 21.4%; Score 293; DB 10; Length 247;
Best Local Similarity 31.2%; Pred. No. 1.9e-18;
Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;

Qy 6 LLYWOLLALFLPFLCQDEYHESQTCG--LPPDCSCCHGDSYFRGYGPPGPPG 63
Db 2 LLLQALLFLUULP-SHAEDDVTTTELAPALVPPPKGTCA-----GWA- -G 45

Qy 64 IPGNHGNNGNNGATGHEGAKGKDGKD- --LGPRGER- --GQHPKGEKGYPCIPPE- - 115
Db | : | | | | | | | | | | | | | | | | | | | | | : | : | : | | |

Qy 46 IPGHSNGNCTPGCRGDRGTGPEKEKGDSGLLGPKEGTGDMGTGARGPRGFGTGPGRKG 105
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Qy 116 -----LQIAFMASLATHFSNQNSGIIFFSVETNIGNFFDMVTGRFGAPVSGVYFFTE 167
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Qy 168 SMKHEDVEVVVYLMHNGNVTFSYSEVMKKGSDTSSNHAVLKLAGDEWILRM-GNG- 225
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Qy 166 HTVYV--MKDVKSFLFKDKKAVLFTYDQYOEKNVDQASGVLLHLEVGQVWLQVYGDG 223
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RESULT 13
US-09-922-598-47
; Sequence 47, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boststein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

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;; PRIOR FILING DATE: 1998-07-09

Query Match 21.3%; Score 290.5; DB 9; Length 259;
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Db 167 PLRGIYFFSLNV--HSNNYKETYVHMHNOKEAVILYA-OPSEERSIMQSOSVMDLAYGD 223
QY 217 EWLIRM-----GNGALHGDHQRFTFAGFL 242
Db 224 RVWVRLFKRQRENATYSNDFDTYITFSGLHI 254

RESULT 14
US-09-989-293A-47

; Sequence 47, Application US/09989293A
; Patent No. US2002017164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; PRIOR FILING DATE: 2001-11-20
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Query Match      21.3%  Score 290.5;  DB 9;  Length 259;
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Mon Jan 13 10:56:36 2003

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